

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number: 141260

TO: Anish Gupta

Location: REM-3C15&3C18

Art Unit: 1654

Wednesday, December 29, 2004

Case Serial Number: 09/823418

From: Edward Hart

Location: Biotech-Chem Library

REM-1A55

Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Gupta,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches. Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions

.rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case .



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STiC-Biotech/ChemLib

41260

From:

Gupta, Anish

Sent:

Monday, December 27, 2004 2:39 PM

To: Subject: STIC-Biotech/ChemLib RE: search request

Serial Number: 09 / 823418

Art Unit: 1654

Room:

Remsen 3C15 Mailbox Room: Remsen 3C18

Please search sequence ID No. 2, 3, 4, 5, 6, 7, 8, 13 and 14

Anish Gupta 2-0859 Remsen.

Protein Sequence Searches - 10/8/04

All of the sequence databases on the ABSS have been updated. A change has occurred in the protein databases.

- Two protein databases, SPTREMBL and SwissProt, are now produced as a single, merged database called UniProt.
- Results from UniProt have the file extension .rup.
- Sequences in UniProt are identified by the same ID that had been used in SPTREMBL or SwissProt.
- In instances where the database curators have determined that an SPTREMBL record and a SwissProt record represent the same sequence, the two records have been merged into one. Both: IDs are present in the record. Any differences found between the two sequences are recorded in the FT (feature table) fields.

If you have any questions regarding these changes or your results, please contact any STIC searcher.

STAFF USE ONLY	
Searcher:	129/84 29/94
Online Time:	

Type of Search	
NA Sequence: #	
AA Sequence :#	L
Structure: #	_
Bibliographic:	
Litigation:	
Patent Family:	
Other:	

Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS:_ SEQUENCE SYSTEM: WWW/Internet:_ Other(Specify):_

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STIC SEARCH RESULT FEEDBACK FORM

IBIO GENERAL MONTH AND THE

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

Yoluntary Results Feedle
> I am an examiner in Workgroup: Example: 1610
> Relevant prior art found, search results used as follows:
☐ 102 rejection
103 rejection
Cited as being of interest.
Helped examiner better understand the invention.
Helped examiner better understand the state of the art in their technology.
Types of relevant prior art found:
☐ Foreign Patent(s)
 Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
> Relevant prior art not found:
Results verified the lack of relevant prior art (helped determine patentability).
Results were not useful in determining patentability or understanding the invention.
Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aay30683 Apo-B100					'n	Aaw57207 Apo B 100	Aaw41261 Apolipopr	N	Abj37575 Heparin b	8 Apo B	Aaw57209 Apo B 100	c	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo		Aaw41262 Apolipopr	Aaw96826 Amino aci	Aau98981 Human apo
ID	AAY30683	AAY30682	AAY30686	AAY30687	AAY30685	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981
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ALIGNMENTS

Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Ŕ AAY30683 standard; peptide; 10 98US-0077618P. 99WO-US004805. Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 AAY30683; RESULT 1 AAY30683

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Sequence 10 AA;

us-09-823-418-2.rag

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AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerobais. The peptides are derived from aminon acids 3358 to 3367 of apoBl00. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which atheroselerosis. The transgenic non-human animals and mammals which atheroselerosis, and in vivo assay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atheroselerotic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3158 to 3167 of apoB100. The method compouse are derived from amino acids 3158 to 3167 of apoB100. The method compouses detecting compounds which affect can be used for identifying compounds with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDD-PG binding withbut inhibiting LDD receptor binding. Such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which capress human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDD-PG binding. They can also be used to identify compounds which result in an increase in also be abarticular food or drug compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 43; DB 2; Length 10;
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.06
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.0%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 90.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0×2×5×8×
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AAY30685 standard; peptide; 10 AA.

RESULT 5 AAY30685 ID AAY30

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us-09-823-418-2.rag

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that last least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKUKHRH (1) or TRRITKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 43; DB 2; Length 11;
Pred. No. 0.072;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                             Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 52; 73pp; English.
                                                                                                                                                                         97WO-GB002610.
                                                                                                                                                                                                         96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1998 (first entry)
                                                                                                                                                                                                                                        (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Conservative
                                                                                                                                                                                                                                                                           Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRLTRKRGLK 11
                                                                                                                                                                                                                                                                                                            WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Modified-site
                                                                                                                                                                                                         27-SEP-1996;
                                                                                                     WO9813385-A2
                                                                                                                                     02-APR-1998
                                                                                                                                                                                                                                                                          Halbert GW,
                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57207;
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The present sequence represents a specifically claimed Apo B 100 binding naturally occurring, receptor-competent low density lipportectal (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sete for an apo B protein receptor and at least 1 of the present of the present of the peptides containing an apo B binding sequence with at least 10% identry with sequences: KAEYKKWKHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-tergeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete app B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                     Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86.0%; Score 43; DB 2;
90.0%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            affinity to an apo B protein receptor
                                                                                                                                                           Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW41261 standard, peptide, 15 AA.
                                                                                                                                                                                                                                                                                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apolipoprotein B-100 fragment.
                                                               97WO-GB002610
                                                                                             96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-GB001255.
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                                                                                                                                                                                                                                                         that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                           (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                         Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prothrombinase complex.
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                                                                                                                                                                                         WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13 AA;
 WO9813385-A2
                                                            25-SEP-1997;
                                                                                             27-SEP-1996;
                              02-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW41261;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
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(ETHZ-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                엄
                                                                                                                                                                                                This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100) Z1-KAQ-X1-KKNKIRHS-X2-T-Z2 (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, apparate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits chibits active as such or as part of a 98-aa peptide, inhibits active as such or as part of a 98-aa peptide, inhibits active as such or as part of a 10-aa prevents activation of activation of the surface of thromboplastin and of platelets by thrombin. It binds to the residues $8.66 of thromboplastin and of platelets by thrombin. Smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                  Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.0%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.1; ive 0; Mismatches 1; Indels
(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore JP;
                                                                                                                                                                     Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96892 standard; peptide; 15 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRDRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRLTRKRGLK 10
                                                                   WPI; 1998-008798/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 9; Conserv
                                   Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96892;
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human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apportein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthitis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                     AAW96878-97 represent nuclear localisation signal sequence derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86.0%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.1; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heparin binding peptide sequence #28.
                                                                                             Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  retinopathy and hypoxia.
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UNIV ZURICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15 AA;
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                                               treatment.
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Length 22;

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Matches
                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 bending site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKNKHRH (1) or TTRLTRREGIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally accounting, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                ö
                                                                                                                                                                                                                                                     Apo B, binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                 Gaps
                                                                ò
                                          Length 20;
                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                             'note= "attached to retinoic acid"
                                                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                   /note= "attached to cholesterol"
                                          DB 6;
                                          Score 43; DB 6;
Pred. No. 0.14;
                                                               0; Mismatches
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                                                                                                                                                                AAW57208 standard; peptide; 22 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    97WO-GB002610
                                                                                                                                                                                                                                                                                                                                                                                                                                                          96GB-00020153
                                         86.0%;
90.0%;
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                                                               9; Conservative
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                                                                                      1 TRLTRDRGLK 10
                                                                                                   7 TRLTRKRGLK 16
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                                        Query Match
Best Local Similarity
                     Sequence 20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22 AA;
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Modified-site
                                                                                                                                                                                                                                                                                                                                                        Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Halbert GW,
                                                                                                                                                                                                                                                                                                  Synthetic.
invention
                                                                                                                                                                                       AAW57208;
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                                                                                                                                              RESULT 11
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipporotein (LDL) particle of the present invention. The LDL particle comprises at least 1 ceptide component that has at least 1 binding site for an apo B protein ceptide component that has at least 1 binding site for an apo B protein ception and at least 1 lipophilic substituent. Also described in the receptor and at least 1 lipophilic substituent. Also described in the competing with sequences: KABYKKWKHRH (1) or TTRLIRKRGLK (2), or their consers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally cocurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                           Gaps
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                                                           1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "attached to retinoic acid"
Score 43; DB 2;
Pred. No. 0.15;
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90.0%; Pred. No. 0.15;
iive 0; Mismatches
                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                           Ä.
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                                                                                                                                                                                                                                                                                                                        AAW57209 standard; peptide; 22
86.0%;
90.0%;
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                                                           9, Conservative
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                                                                                                                    1 TRLTRDRGLK 10
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Best Local Similarity
  Query Match
Best Local Similarity
Matches 9; Conserv
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Modified-site
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AAE14541;

RESULT 13

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AAE14541

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AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major approtein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or inboxme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                           Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus
                     Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.0%; Score 43; DB 2; Length 36; 90.0%; Pred. No. 0.26;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW64587 standard; peptide; 37 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                               97US-00874807.
98US-00079030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 36 AA;
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                            WO9856938-A1
                                                                                                                                                                                                                                                                                                                    10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-0CT-1998
                                                                                                                                                                                                                                                                                                                                                               13-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                        Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           samble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0; Mismatches
                                                                                                                                                                                                                                               Human apoB-100 derived peptide p62.
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                                                                                                             AAE14541 standard; peptide; 34 AA
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7 TRLTRKRGLK 16
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Matches 9; Conserv
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                                                                                                                                                                                                     17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                 peptide p62
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Gaps

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AAW96876;

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RESULT 14 AAW96876

Query Match

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(IMMO) IMMUNO AG.
                                                      13-JAN-1997;
                          12-JAN-1998;
12-AUG-1998,
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98EP-00890007. 97AT-00000044.

Schenk V; Lang H, Moritz B, Kiessig S,

WPI; 1998-416142/36.

Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.

Example 2; Page 9; 18pp; German.

AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain allelss of aposition with hypercysteinsemia and venous thrombosis) and factor VII mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method dees not require complex apparatus for polymerase particularly suited to routine screening. It also allows mutant protein a sample to be quantified

Sequence 37 AA;

. 0 86.0%; Score 43; DB 2; Length 37; 90.0%; Pred. No. 0.27; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0.

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Gaps

1 TRLTRDRGLK 10

11 TRLTRKRGLK 20

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Search completed: December 29, 2004, 12:28:47 Job time : 63.0227 secs

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RESULT 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: qeneseqp1980s:*
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geneseqp1990s:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               geneseqp2000s:*
geneseqp2001s:*
                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                 US-09-823-418-3
48
1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                        Perfect score:
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                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp20028;* geneseqp2003a8;* geneseqp2003b8;* geneseqp20048;*

SUMMARIES

	Description	Aay30684 Apo-B100	Aay30686 Apo-B100	Aay30685 Apo-B100		Aay30687 Apo-B100	Aaw57205 Apo B bin	Aaw57207 Apo B 100	Aaw41261 Apolipopr	Aaw96892 ApoB-100	Abj37575 Heparin b	Apo	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #		Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo	Aay31237 Human Apo	Aaw41262 Apolipopr	Aaw96826 Amino aci	Aau98981 Human apo
	DI			AAY30685	AAY30682	AAY30687	AAW57205		AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687		AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981
	BB	7	0	~	N	0	0	01	7	N	9	0	7	ß	7	0	~	4	4	7	7	8	7	7	7	ស
	Match Length DB	10	10	10	10	10	11	13	15	15	20	22	22	34	36	37	21	343	343	377	377	2463	3923	4536	4536	4560
* 2	Match	100.0	93.8	91.7	89.6	9.68	9.68	89.6	89.6	9.68	9.68	9.68	89.6	89.6	9.68	9.68	89.6	9.68	9.68	89.6	89.6		89.6		9.68	9.68
	Score	48	45	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

Add48677 Human Pro Aao15893 Human apo	Abr40253 Human ali Abn79140 Apolipopr		Human	Adnies/O Human apo Ado33445 Human apo	Ado33447 Human apo	Aau33184 Novel hum	Aay30683 Apo-B100	Aay30690 Apo-B100	-	-	-	Aaw87717 Analogue	Aae21732 BSMR effe	Abu07938 Apoprotei	Adf56451 Human apo	Aaw41260 Apolipopr
ADD48677 AAO15893	ABR40253 ARI79140	ADF43408	ADH18871	ADH18870 ADO33445	AD033447	AAU33184	AAY30683	AAY30690	AAY30692	AAY30688	AAW57206	AAW87717	AAE21732	ABU07938	ADF56451	AAW41260
561	4563 6	563	m r	563	563	4590 4	10 2		10 2	10 2	11 2		11 5		11 7	12 2
9.9	9.68	9.6	9.6	و ب	9	9.	87.5	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2	79.2
4. 4. 6. 6.	4 4 3	43	4 6	4, 4, J. E.	43	43	42	38	38	38	38	38	38	38	38	38
26 27	28 29	30	31	333	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. ġ Claim 17; Page 57; 70pp; English. AAY30684 standard; peptide; 10 98US-0077618P. 99WO-US004805. Innerarity TL, Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999, AAY30684; AAY30684 2

Sequence 10 AA;

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AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate attenoselerosis. The peptides are derived from aminon acids 1358 to 336 of apoBl00. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotis and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can subso used to identify compounds which result in an increase in a therosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the constitution of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                                                                                           100.0%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.0073; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                       AAY30686 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0077618P.
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                                                                                                                                                                                                                                                         1 TRLTRARGLK 10
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les 10; Conserv
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate attensoslerosis. The peptides are derived from amino acids 3358 to 336 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in also be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the command of a therosclerosis in an animal or mammal reducing the severity of atherosclerosis in an animal or mammal
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   Length 10;
                                     0; Indels
 Score 45; DB 2;
Pred. No. 0.03;
1; Mismatches (
                                                                                                                                                                                       AAY30685 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US004805.
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   93.88;
                 90.06;
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Best Local Similarity 90.vv
                                   9, Conservative
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                                                                    1 TRLTRARGLK 10
                                                                                        TRLTRSRGLK 10
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Query Match
Best Local Similarity
Matches 9; Conserv
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AAY30685
ID AAY3
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Gaps

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Length 10; 1; Indels

91.7%; Score 44; DB 2; 90.0%; Pred. No. 0.047; ive 0; Mismatches

1 TRLTRARGLK 10

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(first entry)

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosele-rosals. The peptides are derived from amino acids 3158 to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which hisrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which herebuller atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in also be used to identify compounds which result in an increase in also be aparticular food or drug composition tends to stimulate or inhibit the companion of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                 Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                              Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoBl00. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the commation of atherosclerosic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                                                                                                               Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                            Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                              AAY30682 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US004805
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Best Local Similarity 90.0
Matches 9; Conservative
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TRLTRTRGLK 10
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                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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99WO-US004805. 98US-0077618P.

Boren JOS;

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                                     Gaps
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                  Score 43; DB 2; Length 10;
Pred. No. 0.076;
0; Mismatches 1; Indels
                                                                                                                                AAW57205 standard; peptide; 11 AA.
                  89.6%;
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       Query Match
Best Local Similarity 90.vv,
Best Local Similarity
                                                                                                                                                                          03-AUG-1998 (first entry)
                                                           1 TRLTRARGLK 10
                                                                              1 TRLTRORGLK 10
Sequence 10 AA;
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Gaps

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1; Indels

TRLTRARGLK 10 TRLTRERGLK 10

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AAY30687 standard; peptide; 10 AA.

RESULT 5 AAY30687 ID AAY30

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96GB-00009702
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      WO9813385-A2
                                                    25-SEP-1997;
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                           02-APR-1998.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TRRITRKRGLK (2), or their dimers. Non-sequences: KAEYKNKHRHH (1) or TRRITRKRGLK (2), or their dimers. Non-that express an apo B protein receptor, and (ii) additives for cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                          Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide B.
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                                                                                                                                                                                               Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57207 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                          Claim 12; Page 52; 73pp; English.
                                                                                                                       97WO-GB002610.
                                                                                                                                              96GB-00020153.
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                                                                                                                                                                     (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                             Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRARGLK 10
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Modified-site
                                                                                                                                              27-SEP-1996;
                                                                      WO9813385-A2
                                                                                               02-APR-1998
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Matches
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARKKANKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer calls that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                       Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Fig 7; 73pp; English.
97WO-GB002610
                                                                                                96GB-00020153
                                                                                                                                                                                                 (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                  Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-230637/20.
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Score 43; DB 2; Pred. No. 0.098; 0; Mismatches 89.6%; Local Similarity 90.0 les 9; Conservative 1 TRLTRARGLK 10 12

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Gapa

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Length 13; 1; Indels

> AAW41261 standard; peptide; 15 AA. Apolipoprotein B-100 fragment. (first entry)

Anti-coagulant, apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14; 97WO-GB001255 prothrombinase complex.

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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (I) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids as , Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, as peptate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-as peptide, inhibits which he prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of the residues 58-66 of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclerosis.
                                                                                                        Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 43; DB 2; Length 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         smaller than apoB-100, they act more quickly
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(UNLO ) ROYAL FREE HOSPITAL SCHOOL MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore JP;
                                                                                                                                                                                  Disclosure; Page 22; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW96892 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.68;
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                                    Ettelaie C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guevara JG, Hoogeveen RC,
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Matches 9; Conservative
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                                                                     WPI; 1998-008798/01.
                                 Bruckdorfer KR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15 AA;
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WPI; 1999-070331/06

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                                                                                                          AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vito, for expressing a therapeutic polypetide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic, antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatcid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maynard HD;
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                                                                            Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37575 standard; peptide; 20 AA.
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                                                                                                                                                                                                                                                                                                                                 fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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                                        treatment.
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Gaps

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AAW57208 standard; peptide; 22 AA.
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                                                                                    03-AUG-1998 (first entry)
                          9; Conservative
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                                   1 TRLTRARGLK 10
                                            7 TRLTRKRGLK 16
                                                                                                                                                                                                                 WPI; 1998-230637/20.
                Query Match
Best Local Similarity
         Sequence 20 AA;
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                                                                                                                                Key
Modified-site
                                                                                                                                              Modified-site
                                                                                                                                                           WO9813385-A2
                                                                                                                                                                             25-SEP-1997;
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                                                                                                                       Synthetic.
invention
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKOKHRH (1) or TTRLINGROIM (2), or thair dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticencer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for courring, receptor-competent LDL particles and (ii) additives occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                Score 43; DB 2; Length 22; Pred. No. 0.17;
                                                            1; Indels
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89.6%; Scor.
90.0%; Pred. No. o....
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         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                  1 TRLTRARGLK 10
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                                                                                                                                             7 TRLTRKRGLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
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                                                                                        Score 43; DB 6; Length 20;
Pred. No. 0.15;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "attached to retinoic acid"
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                                                                                        89.6%;
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Query Match 89.6%; Score 43; DB 2; Length 22; Best Local Similarity 90.0%; Pred. No. 0.17; Matches 9; Conservative 0; Mismatches 1; Indels

Sequence 22 AA;

1 TRLTRARGLK 10

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AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (ILDL), low density lipoproteins (LDL) and lipoprotein a. The present specification describes a composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollpoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.27;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 16; Fig 12C; 293pp; English.
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                                                                                                                                                                                                                                                                                                                                 (BAYU ) BAYLOR COLLEGE MEDICINE.
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98US-00079030.
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                                                                                                                                                                                                                                          10-JUN-1998;
                                                                                                                                         Homo sapiens
                                                                                                                                                                       WO9856938-A1
                                                                                                                                                                                                                                                                            13-JUN-1997;
                                                                                                                                                                                                                                                                                                14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-OCT-1998
                                                                                                                                                                                                          17-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EP857973-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW64587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BXSXXXXXXXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to peptides having affinity for oxidised low density lipoprotein (OxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for OxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a partient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                      Oxidised low density lipoprotein; oxLDL, immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.6%; Score 43; DB 90.0%; Pred. No. 0.26 iive 0; Mismatches
                                                                                                                                                                                       Human apoB-100 derived peptide p62.
                                                                                 AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 90.0
7 TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRARGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-179777/23.
                                                                                                                                                                                                                                                                                                                                             WO200206314-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                              peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lipoprotein.
                                                                                                                                                   17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                   24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Narvanen O,
                                                                                                                   AAE14541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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Gaps ö

Length 36; 1; Indels

Score 43; DB 2;

us-09-823-418-3.rag

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12-AUG-1998
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98EP-00890007. 97AT-00000044. Moritz B, Kiessig S, (IMMO) IMMUNO AG. 12-JAN-1998; 13-JAN-1997,

Schenk V; Lang H, WPI; 1998-416142/36.

Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.

Example 2; Page 9; 18pp; German.

AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apol indicates increased risk of developing Alzheimer's disease), thermostable 5.10-methylenetetrahydrofolate reductas cassociated with hypercysteinaemia and venous thrombosis) and factor VII method can also be applied to proteins from pathogenes, e.g. viruses or pathod one and to require complex apparatus for polymerase contain reactions, it is simple, standardisable and reliable and is a sammla by manial to be manial to be manial to be associated to routine screening. It also allows mutant protein particularly suited to routinin a sample to be quantified

Sequence 37 AA;

Gaps ; 89.6%; Score 43; DB 2; Length 37; 90.0%; Pred. No. 0.28; Live 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0
Matches 9, Conservative

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1 TRLTRARGLK 10

||||| |||| 11 TRLTRKRGLK 20

S S ð

Search completed: December 29, 2004, 12:28:48 Job time : 62.0227 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57 ; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec ë:

US-09-823-418-3 1 TRLTRARGLK 10 Perfect score: Sequence:

BLOSUM62 Scoring table:

283416 segs, 96216763 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl: pir2:* pir3:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Descript	apolipoprotein B -			apolipoprotein B -	acetyltransferase,	apolipoprotein B-1	conserved hypothet	hypothetical prote	pyruvate dehydroge	ULS6 protein - hum	hypothetical 34.6	hypothetical prote		$\overline{}$	probable membrane	apolipoprotein B-1	hypothetical prote	cruciferin 1 precu	probable two-compo	apolipoprotein B-1	hypothetical prote	Na+/K+-exchanging	polyketide synthas	ISU ribosomal prot	hypothetical prote	phosphoadenylyl-su	hypothetical prote		conserved hypothet
SUMMARIES	Д	S32802	LPHUB	C60950	JH0102	G87383	E60950	AH0906	E72514	DEHUPT	C48560	E65112	E85985	B91140	D96795	855958	A60950	D70975	A35540	D83041	JH0101	T32744	T18833	T17409	G90222	H70665	S28609	E83363	S39854	AE0432
	DB	2	~	~	~	~	7	N	N	н	-	Н	~	~	~	~	~	~	~	7	N	~	~	~	7	~	Н	N	N	7
		596	4563	269	779	173	275	309	208	388	233	309	309	309	398	171	274	387	509	542	784	829	1049	4613	216	225	232	272	290	307
df	Query Match	89.6	9.68	81.2	81.2	77.1	77.1	•	72.9	72.9	70.8	70.8	70.8	70.8	70.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	68.8	66.7	66.7	66.7		66.7	66.7
	Score	43	43	39	39	37	37	36	35	35	34	34	34	34	34	33	33	33	33	33	33	33	33	33	32	32	32		32	32
		-	7	٣	4	Ω	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29

leucine rich repea	probable aminotran	probable phosphopr	clpx (AF218420) [i	ATP-dependent Clp	probable thiophene	tRNA modification	flagellum-specific	H+-transporting tw	flagellum-specific	H+-transporting tw	DNA repair protein	starch synthase (E	H+-transporting tw	probable ppdK prot	flagellum-specific
T17033	D83057	S48288	F97512	AF2731	P97698	AG2924	AE0752	C42364	H90963	B64958	B87455	S40051	AI0222	H70538	Н85811
7	~	~	~	7	7	~	7	7	~	7	7	N	~	N	0
329	390	393	425	425	442	442	456	456	457	457	460	484	484	490	496
66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7	66.7
32	32	32	32	32	32	32	32	32	32	32	32	32	32	32	32

ALIGNMENTS

apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S32802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Punk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchin Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: S32802
A;Accession: S32802
A;Accession: preliminary

A;Molecule type: mRNA A;Residues: 1-596 <PAP> A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301 C;Superfamily: apolipoprotein B

Gaps ö Score 43; DB 2; Length 596; Pred. No. 0.76; 1, Indels 0; Mismatches 89.6%; Query Match Best Local Similarity 90.0 Matches 9; Conservative

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226 TŘLTŘKŘĠĽK 235 1 TRLTRARGLK 10 g

8

RESULT 2

apolipoprotein B-100 precursor

N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27860; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A2752; 161909; 159510; 139474; 139469; 184624; 137179; PS0058
R;Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc. DNA 6; 363-372, 1987

A;Title: DNA sequence of the human apolipoprotein B gene.

A;Title: DNA sequence of the human apolipoprotein B gene.

A;Reference number: A27850; MUID:88003974; PMID:3652907

A;Rocession: A27850

A;Rocession: A27850

A;Rocession: L-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'A;Residues: L-617,'A',619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'Q',3433-3731,'A;Rocession: Exercices: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:O9UMNO; UNI:

B;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.

EMBO J. 5, 3495-3507, 1986

A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r:

A;Reference number: A91058; MUID:87161758; PMID:3030729

A;Reference number: A91058; MUID:87161758; PMID:3030729

A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 < CLA>

A;Residues: 1-11,15-2739,'S',2541-3823,'R', Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC.

Nucleic Acids Res. 14, 7501-7503, 1986

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Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Atherosclerosis 58, 277-289, 1985
Ayritle: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A; Reference number: A90084; MUID:86130855; PMID:3841481
A; Accession: A29287
A; Accession: A29287
A; Accession: A29287
A; Asecular type: mRNA
A; Residues: 3846-4298 <SHO>
B; Pfitzner, R.; Wagener, R.; Stoffel, W.
B; Pfitzner, R.; Wagener, R.; Stoffel, R.; Mille, R.W.; Li, W.H.; Sparrow, J.T.; R.; M.; C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.; Proc. Natl. Accession: A4738; MUID:86042646; PMID:2932736
B; Accession: A4738; MUID:86042646; PMID:2932736
B; Accession: A4738; MUID:86042646; PMID:2932736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AjMolecule type: mRNA
AjResidues: 'N' 3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
AjCross-references: GBM12413; NID:g178795; PIDN:AAA51742.1; PID:g178736
RjChen, S.H.; Habib, G; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cail
Science 238, 363-366, 1987
AjTitle: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Accession: 840133
A, Accession: 840133; MUID:88018019; PMID:3659919
A, Accession: B40133
A, Accession: B40133
A, Cross-references: GB:M18036; NID:9178799; PIDN:AAA51754.1; PID:9178800
A, Cross-references: GB:M18036; NID:9178799; PIDN:AAA51754.1; PID:9178800
A, Accession: A40133
A, Accession: A40133
A, Accession: A40133
A, Molecule type: protein
A, Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55;
A, Molecule type: protein
A, Residues: 51-75;101-110;129-139;158-174;197-207;276-287;298-304;306-314;526-532;538-55;
A, Molec: these fragments were derived from apode
R, Hardman, D.A.; Protter, A.A.; Schilling, J.W.; Kane, J.P.
Biochem: Blophys. Res. Commun. 149; 1214-1219; 1987
A, Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism planator: A28002; MUID:88106542; PMID:3426612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA A; Residues: 2169-2179 < HOS.
A; Residues: 2169-2179 < HOS.
A; Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, R; Asnay C., Kim, T.W.; Wengy, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Reference number: A35783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Wolecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
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A; Readdudes: 1229-2179; 2181-2235 cHA2>
A; Readdudes: 1229-2179; 2181-2235 cHA2>
A; Experimental source: intestine
A; Experimental source: intestine
A; NOte: this mRNA from intestine includes a stop codon created by RNA editing in place
R; Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.P.; Kirchgessner,
Nucleic Acids Res. 13, 6937-6953, 1985
A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A; Accession: A24269; MUID: 86041888; PMID: 3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stop codon in human intestine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 3056-3159 < MEH>
A; Cross-references: GB:X03045; NID:9287B3; PIDN:CAA26850.1; PID:9929609
A; Cross-trankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.
Biochem. Blophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in
A; Reference number: A29659; MUID:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A29659
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AyAccession: A.297 - Ay Mount.

AyAccession: A.296 - AyAccession.

AyAccession: A.2967 - AyAccession.

AyAcc
                                                                                               A,Accession: A25263
A,Anlecule type: mRNA
A,Molecule type: mRNA
A,Febdidues: 1-272, Nv, 274-617, A, 619-1217, E, 1219-2091, Vv, 2093-2364, T', 2366-2679, 'Q'
A,Cross-references: GB:X04506, NID:g34330, PIDN:CAA28191.1; PID:g34331
B,Co. WH, Grant, S, M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad Sci. U.S.A. 83, 8142-8146, 1986
A,Title: Human liver apolipoprocein B-100 cDNA: complete nucleic acid and derived amino
A,Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-617, A',619-703, P',705-792, R',794-1270, S',1272-1866, G',1868-2036, N',2
4189-4220, M',422-4563 <LAM>
A,Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
R;Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
A,Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A;Reference number: A92556, MUID:87008488, PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-97, '1', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
9-4132, 'G', 4134-4180, 'E', 4182-4563 - CHES.
A; Cross-references: GB:J02610; NID:9178803; PIDN:AAA35549.1; PID:9178804
A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
F; Protter: A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad Sci. US.A. 83, 5678-5682, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A; Accession: A24320; MUID:86287319; PMID:3461454
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A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Cross-references: GB: M12480; NID: 9178791; PIDN: AAA51751.1; PID: 9178792
R; Protter: A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki Protc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopx A; Reference number: A94088; MUID: 86149325; PMID: 3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-97, 1', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138,' PTGRLPNCFSNGLICYSLWLHSFQE
A; Cross-references: GBH4081, NTD:91/89795, PIDN:AAA51752.1; PID:9553189
R; Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor,
Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of
A; Reference number: A24684; MUID:86094221; PMID:3001697
A;Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A;Reference number: A93639; MUID:87016385; PMID:3763409
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Cispecies: Mesocricctus auratus (golden hamster)
Cispecies: Mesocricctus auratus (golden hamster)
Cispecies: Mesocricctus (golden hamster)
Cispecies: Mesocricctus (golden hamster)
Cispecies: Mesocricctus (golden hamster)
Cispecies: Miles (golden hamster)
Sismith, T.J.
submitted to GenBank, June 1990
Aireference number: A3864
Aireference: JH0102
Aireferences: UNIPROT: C60536; GB: M35187
Aireference: WINPROT: C60536; GB: M35187
Aireference: Miles a revision to the sequence from reference JH0101
Bismith, T.J.; Hautamaa, D.; Maeda, N.
Airitle: Sequence of the putative low-density lipoprotein receptor-binding regions of an Aireference number: JH0101; MUID: 90236327; PMID: 2332175
Aireference number: JH0101; MUID: 90236327; PMID: 2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Genetics:
A;Gene: apoB
A;Gene: apolipoprotein B
C;Keywords atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       actyltransferase, GNAT family [imported] - Caulobacter crescentus
C;Species: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87383
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J
B; Laub, M.T.; DeBoy, K.T.; Dodson, K.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo,
n, J; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87383
A;Residues: preliminary
A;Molecule type: DNA
A;Residues: 1-173 <STO>
A;Cross-references: UNIPROT:Q9A9B1; GB:AE005673; NID:g13422385; PIDN:AAK23067.1; GSPDB:C;Genetics:
A;Gene: CC1083
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C;Species Gallus gallus (chicken)
C;Species 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: E60950
E;Law, A.; Scott, J.
J. Lipid, Res. 31, 109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 779;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 2;
Pred. No. 6.5;
1; Mismatches
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                                         apolipoprotein B - golden hamster
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Best Local Similarity 80.0%;
Matches 8; Conservative
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                     apolipoprotein B-100 - golden hamster (fragment)

C.Species: Mesocricetus auratus (golden hamster)

C.Species: Mesocricetus auratus (golden hamster)

C.Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C.Accession: C60950

J. Lipid Res. 31, 1109-1120, 1990

A.Rilaw, A.; Scott, J.

J. Rose-species comparison of the apolipoprotein B domain that binds to the LDI
A.Reference number: A60950; MUD: 90324804; PMID: 2373961

A.Reference number: A60950; MUD: 90324804; PMID: 2373961

A.Residues: 1-269 <LAM.
A.Residues: 1-269 <AM.
A.Residues: 1-260 <AM.
A.Residues: 1-2004 <AM.
A.Residues: 1-2004 <AM.
A.Residues: 1-2004 <AM.
A.Residues: 1-2004 <AM.
A.Residu
           26
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.B.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS. Lett. 170, 105-108, 1984
A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
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81.2%; Score 39; DB 2; Length 269;
Best Local Similarity 80.0%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels
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216 SRLTRKRGLK 225
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Best Local Similarity
Matches 9; Conserv
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A/Genee: GDB:PDHA2
A/Cross-references: GDB:120711; OMIM:179061
A/ABQ position: 4022-4423
A/Cross-references: GDB:120711; OMIM:179061
A/ABQ position: 4022-4423
A/ABQ position: 4022-4423
C/Superfamily: pyruvate dehydrogenase (lipoamide) alpha chain; thiamin pyrophosphate-bin F/1-27/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F/18-3-232/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F/183-232/Domain: thiamin pyrophosphate-binding domain homology <TPB>
F/230/Binding site: phosphate (Ser) (covalent) #status predicted
F/230/Rinding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                             pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain precursor, testis-specific - N.Alternate names: pyruvate dehydrogenase complex, El component alpha chain
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R;Rosen-Wolff, A.; Frank, S.; Raab, K.; Moyal, M.; Becker, Y.; Daral, G.
K;Rosen-Wolff, A.; Erank, S.; Raab, K.; Moyal, M.; Becker, Y.; Daral, G.
A;Tura Res. 25, 189-199, 1992
A;Title: Determination of the coding capacity of the BamHI DNA fragment B of apathogenic A;Roference number: A48560; MUID:93070559; PMID:1332274
                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
C;Accession: A37104
R;Dahl, H:M.; Brown, R.M.; Hutchison, W.M.; Maragos, C.; Brown, G.K.
Genomics 8, 225-232, 1990
A;Title: A testis-specific form of the human pyruvate dehydrogenase Elalpha subunit is A;Reference number: A37104; MUID:91065637; PMID:2249846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-388 <DAH>
A;Cross-references: UNIPROT:P29803; GB:M86808; GB:J04769; NID:g190789; PIDN:AAA60232.1;
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C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
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A,Residues: 1-233 <ROS>
A,Residues: U-233 <ROS>
A,Cross-references: UNIPROT: P36297
A,Note: sequence extracted from NCBI backbone (NCBIN:117573, NCBIP:117577)
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C,Superfamily: herpesvirus UL56 protein
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                                                        2 RLTRARGLK 10
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Best Local Similarity
8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Androved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 #SAccession: AH0906 R;Parkhill, J; Dougan, G; James, K.D; Thomson, N.R; Pickard, D; Wain, J; Churcher, H, T.; Connerton, P; Cronin, A; Davis, P; Davise, R.M; Dowd, L; White, N.; Farrar, S, Moule, S; Quall, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A, Reference number: AB0502; MUID:21534947; PMID:11677608
A;Retus: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <- PAR>
A;Residues: 1-309 <- PAR>
A;Residues: 1-309 <- PAR>
A;Residues: 1-309 <- PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
                         A/Accession: E60950
A/Accession: E60950
A/Molecule type: mRNA
A/Molecule type: L-275 < LAM>
A/Cross-references: UNIPROT: 07LZ77
C/Superfamily: apolipoprotein B
C/Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein APE2090 - Aeropyrum pernix (atrain K1)
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Species: Aeropyrum pernix
C;Accession: E72514
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takahyay, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Retus: Preliminary
A;Residues: preliminary
A;Residues: 1-208 < KAW>
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Experimental source: strain Kl
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                                                                                                                                                                                                                                                    Length 275;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical
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A, Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                              77.1%; Score 37; DB 2;
80.0%; Pred. No. 6.3;
tive 0; Mismatches
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72.9%; Score 35; DB
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches
                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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TRIARERGLK 179
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A;Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:c
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
Genetics:
A;Gene: EC94090
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dyobble DnaJ protein, 19794-17391 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: D56795
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Cinn, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.P.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.P.; Hughes, B.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziall, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: D56795
A;Accession: D56795
A;Accession: D56795
A;Accession: D56795
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A;Residues: 1-398 <STO>
A;Cross-references: UNIPROT:Q9SRE3; GB:AE005173; NID:g6143904; PIDN:AAF04450.1; GSPDB:G
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A;Molecule type: DNA
A;Residues: 1-171 - ADUZ.
A;Eesidues: 1-171 - ADUZ.
A;Cross-references: UNIPROT:006057; EMBL:U19729; NID:g625097; PID:g625102; GSPDB:GN0001
A;Experimental source: strain S288C (AB972)
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C;Species: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: 855958
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                                                                                                                                                                                                                                                              Score 34; DB 2; Length 309;
Pred. No. 29;
1; Mismatches 2; Indels
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C;Keywords: transmembrane protein
F;24-40/Domain: transmembrane #status predicted <TM1>
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A; Description: The sequence of S. cerevisiae cosmid 8084.
A; Reference number: 855944
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Best Local Similarity 70.0%;
Matches 7; Conservative
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A,Cross-references: SGD:S0004394
A,Map position: 12R
C,Superfamily: Saccharomyces pro)
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Best Local Similarity 100.
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                                                                                                             Riblatiner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc. A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Feference mumber: A64720; MUID:97426617; PMID:9278503
A.Status: preliminary; nucleic acid sequence not shown; translation not shown A; Status: DNA A; Residues: 1-309 < BLAT>
A; Residues: 1-309 < BLAT>
A; Residues: UNIPROT:P45476; GB:AE0000400; GB:U00096; NID:g2367203; PIDN:AAC76243.
A; Experimental source: strain K-12, substrain MG1655
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R. Perna, N. T.; Plunkett III. G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew III. G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grobbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A; Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A; Reference number: A85480; MUD:21074935; PMID:11206551
A; Accession: E85985
A; Residuary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residuary

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C;Species: Bacherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: B91140
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: B91140
A;Accession: preliminary
A;Actuue: preliminary
A;Residues: 1-309 <HAY>
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    hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (strain
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A;Gene: yhcC
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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A;Experimental source: strain 0157:H7, substrain EDL933
C;Genetica:
A;Genetica:
A;Gene: yhcc
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                        C.Species: Escherichia coli
C.Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
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Pred. No. 29;
1; Mismatches 2; Indels
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Matches 7; Conservative
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170 TQLARORGLK 179
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170 TQLARQRGLK 179
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Query Match
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Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps
Qy 1 TRLTRARG 8
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Eutheria; Primates; Catarrhini; Hominidae; Homo
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MEDLINE=87161758; PubMed=3030729;
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                   Mammalia, Euther
NCBI_TaxID=9606;
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P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Created)
01-N0V-1986 (Rel. 03, Last sequence update)
05-UUL-2004 (Rel. 44, Last sequence update)
Apollboprocein B-100 precursor (Apo B-100) [Contains: Apollpoprotein Name-APOS).
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MEDLINE=87191999; PubMed=2883086;
CarlaBoon P., Darnfors C., Olofsson S.O., Bjursell G.;
CarlaBoon P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of the B-74 region.";
Gene 49:29-51 (1986).
EMBL: M15421; AAA51758.1; -.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
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Last annotation update)
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO:0006869; P:lipid transporter Activity; NAS.
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PIR; S32802; S32802.
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Submitted (FEB-1992) to
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Homo gapiens (Human). Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,

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"The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
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MEDLINE-9630628; Dubded-2994225;
Knott T.J., Rall S.C. Jr., Innearity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
[10]
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SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-87008488; PubMed=3759943;
Chen S.-H., Yang Chen Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3056-3159 FROM N.A.
SEQUENCE OF 3056-3159 FROM N.A.
MEDINE=86041889; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.,
"Human apollipoprotein B: identification of cDNA clones and
characterization of mRNA.";
Nucleic Acids Res. 13:6937-6953(1985).
SEQUENCE FROM N.A.
MEDLINE=87016385; PubMed=3763409;
MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete CDNA and derived protein sequence of human apolipoprotein
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MEDLINE-86093680; PubMed=3841204;
Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=87041416; PubMed=3464946;
MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lee N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
                                                                                                                                                                                                                                                                                                                                                                         Ludwig E.H., Blackhart B.D., Pierotti V.R., Calati L., Fortier C
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
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"Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
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SEQUENCE OF 709-906 FROM N.A.
SEQUENCE OF 709-906 FROM N.A.
MEDLINE-85270450, PubMed=3860836,
Deeb S.S., Motulsky A.G., Albers J.J.,
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE=88003974; PubMed=3652907;
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VARIANT LEU-2739.
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                     MEDLINE=86149325, PubMed=3513177;
Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kirsher S.W., McEnroe G., Kane J.P., T. Kirsher S.W., McEnroe G., Kane J.P., "Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.", Nature 323:738-742(1986).
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Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88018019; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.,
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
Levy-Wilson B., Scott J.;
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                                                                                                                                                                                            SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE-86287319; PubMed-3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M.
Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of cDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.; "Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
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MEDLINB=20143590; PubMed=10679026;
Shao Y., Mccabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM-BINDING DATA.
MEDLINE=86442245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B is calcium binding protein."; Biochem. Biophys. Res. Commun. 137:493-499(1986).
                                                                                                                         apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                                                                                                                             apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
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MEDLINE=89098975; PubMed=2563166;
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  SEQUENCE OF 1-291 FROM N.A.
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AND LIE-3921.

MEDLINE-98141125; PubMed-9490296;
MEDLINE-98141125; PubMed-9490296;
MEDLINE-98141125; PubMed-9490296;
Mecren T. P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
Screening for mutations of the apolipoprotein B gene causing hypocholesterolemia.,
Hum. Genet. 102:44-49(1998).

- - FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48). LDL (apo B-100) and VLDL (apo B-100).

B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apo8/E receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97044521; PubMed=8889592;
Poirier O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE=91016974; PubMed=2216805; Manan L..S., Gavish D., Breslow J.L.; Bresquence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=97403938; PubMed=9259199;
Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krempf M., Giraudet P., Junien C., Boileau C.,
"Familial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500-->GLN and ARG351-->CYS mutations in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 4563;
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Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.,
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Including Ag(X) antigen).
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0; Mismatches
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                           Clin. Invest. 95:1225-1234(1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR-SSCP.";
Hum. Mutat. 8:282-285(1996)
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Gaps

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Glaucomys volans (Southern flying squirrel).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINES-2761261. PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships ";

Mol. Phylogenet. Evol. 2225-240(2003).

EMBL, AY243379; AAPSO767.1; -.
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Diceros bicornis (Black rhinoceros).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Diceros.
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                                                                                                                                                     Score 43; DB 2; Length 4563;
Pred. No. 36;
0; Mismatches 1; Indels
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                                                                                                                      4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                       421 AA
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07YR10;
07YR10;
01-OCT-2003 (TYEMBLE-1: 25, CX
01-OCT-2003 (TYEMBLE-1: 25, L9
01-OCT-2003 (TYEMBLE-1: 25, L9
                                                                                                                                                    89.6%;
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Best Local Similarity 90.0
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264 SRLTRKRGLK 273
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NCBI_TaxID=64683;
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SEQUENCE 4
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Npolipoproted B 100 (Fragment).
Name=apoB-100;
Nytimene albiventer (Common tube-nosed fruit bat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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MEDLINE=22561261; PubMed=12878460;
MEDLINE=2261261; PubMed=12878460;
Marine-Madsen H., Koepfil, K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationablys.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
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                                                                                            81.2%; Score 39; DB 2; Length 432;
80.0%; Pred. No. 21;
iive 1; Mismatches 1; Indels
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48171 MW; F27B7AB39604732C CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Applipoprotein B 100 (Fragment).
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Mol. Phylogenet. Evol. 28:225-240(2003)
EMBL; AY243375; AAP50763.1; -.
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                                                                                                         Local Similarity 80.0
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279 SRLTRKRGLK 288
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                                                                  432 AA;
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                          Lipoprotein.
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SEQUENCE 436
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SEQUENCE
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SEQUENCE FROM N.A.

MEDLINE-2761261, bubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for euthearian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AF548417; AAP97373.1; -.
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Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker; apolipoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Bvol. 28:225-240(2003).
EmBL; AY243369; AAPS0757.1].
InterPro; IPRO0871; Beta lactamase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                        Agouti paca (Paca).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
NCBI TaxID=108852;
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Mammalia, Eutheria, Rodentia, Hystricognathi, Hydrochaeridae;
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                                    2; Length 445;
                                                                      Indels
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445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
 445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Hydrochoerus hydrochaeris (Capybara) (Carpincho).
                                   81.2%; Score 39; DB 80.0%; Pred. No. 21;
                                                                      1; Mismatches
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288 SRLTRKRGLK 297
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                               Query Match
Best Local Similarity
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NCBI_TaxID=10149;
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445
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SEQUENCE 44
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Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AX243383; AAP50771.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDINE=22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolitopprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Bvol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                      Apolipoprofein B (Fragment).
Rousettus amplexicaudatus (Common rousette).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-077-2003 (TrEMBLrel. 25, Created)
01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Apolloportein B (Fragment).
Chaetophractus villosus (South American armadillo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
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                                                                                                     Score 39; DB 2; Length 438;
Pred. No. 21;
1; Mismatches 1; Indels
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                                                                      48734 MW; 2BD85BCBF4E2CC41 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                     438 AA.
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80.0%;
EMBL; AF548436; AAP97392.1;
                                                                                                   Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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NCBI_TaxID=58083;
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281 SRLTRKRGLK 290
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281 SRLTRKRGLK 290
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438 AA;
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01-077-2003 (TrEMBLrel. 25, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment)
Erethizon dorsatum (North American porcupine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Hystricognathi, Brethizontidae,
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madsen H., Koepfil, K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships.";

MOI. Phylogenet. Evol. 28:225-240(2003).

Lipoprotein. 1 1

NON TER 145 445

SEQUENCE 445 AA; 49617 MW, 9572FESFFSE7625F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=90336327; PubMed=2332175;
Smith T.J., Hautamaa D., Madda N.;
"Sequence of the putative low-density lipoprotein receptor-binding cedons of apolloporotein B in mouse and hamster.";
regions of apolloporotein B in mouse and hamster.";
EMBL, M35187; AAA37059.1; -.
PIR; C60950; C60950.
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060536;
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
Mesocricetus Actazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalais; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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Score 39, DB 2; Length 445;
Pred. No. 21,
1; Mismatches 1; Indels
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445 AA; 49617 MW; 9572FB5F5B7625F2 CRC64;
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780 780
780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                                                                                                                                            445 AA.
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Query Match
Best Local Similarity 80.0%;
Matches 8; Conservative
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288 SRLTRKRGLK 297
                                                     1 TRLTRARGLK 10
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288 SRLTRKRGLK 297
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78
SEQUENCE 780
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Q7TN72
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Query Match

Query Match

Best Local Similarity 80.0%; Pred. No. 38;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TRLEARGLK 10

Db 642 SRLFRRGLK 651
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earch completed: December 29, 2004. 1

Search completed: December 29, 2004, 12:37:30 Job time : 59.5202 secs

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December 29, 2004, 12:10:41 ; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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49
1 TRLTRTRGLK 10
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Perfect score:
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geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:*
geneseqp1990s:*
geneseqp2000s:*
geneseqp2001s:* A_Geneseq_23Sep04:* 1: geneseqp1980s.* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aav30685 Apo-B100			•				Aaw57207 Apo B 100		Aaw96892 ApoB-100	Abj37575 Heparin b		Aaw57209 Apo B 100	g	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo	Aar34031 Sequence	Adj57400 Human apo	Human	Aaw41262 Apolipopr	
SUMMARIES	AAY30685	AAY30686	AAY30684	AAY30683	AAY30682	AAY30687	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826
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Length	101	10	10	10	10	10	11	13	15	15	20	22	22	34	36	37	51	343	343	377	377	2463	3923	4536	4536
% Query Match	100.0	91.8	89.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	87.8	٠	87.8
Score	49	45	44	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43	43		43
Result No.		8	m	4	ß	9	7	80	6	10	11	12	13	14				18							25

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

	Apolip Apolip Human Human Human	Ado33447 Human apo Aau33184 Novel hum Aay30690 Apo-B100 Aay30692 Apo-B100 Aay30688 Apo-B100 Aay57266 Apo B 100	Anal BSMR Apop Huma Apol
AAU98981 ADD48677 AAO15893 ABR40253	ABU79140 ADF43408 ADH18871 ADH18870 ADO33445	ADO33447 AAU33184 AAY30690 AAY30692 AAY30688 AAX30688	AAW87717 AAE21732 ABU07938 ADF56451 AAW41260
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ALIGNMENTS

RESULT	RESULT 1
<u>e</u>	AAY30685 standard; peptide; 10 AA.
Y S	AAY30685;
1	17-NOV-1999 (first entry)
8	Apo-B100 derived peptide showing a proteoglycan receptor mutation.
žž	Apo-B100; proteoglycan receptor mutation; atherosclerosis;
₹	low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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SO	Synthetic.
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Ä	WO9946598-A1.
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PD	16-SBP-1999.
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PF	05-MAR-1999; 99WO-US004805.
X 8	10-Wab-1098. 9817-00-27789.
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PA	(REGC) UNIV CALIFORNIA.
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PI	Innerarity TL, Boren JOS;
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Z X	WPI; 1999-551509/46.
5 E	That i fering commoning which affort hinding of low descripts isoperated
Z 5	With proceedings, used for, e.g. obtaining compounds for reducing
ζ,	ACINGLOSCIALOSIS.
\$ 82	Claim 17: Page 57: 70pp: Rholish.
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ខ	AAY30582-Y30700 represent apo-B100 derived peptides showing proteogl
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႘	modulate atherosclerosis. The peptides are derived from amino acids
႘	to 3367 of apoB100. The method comprises detecting compounds which a
ນ	low density lipoprotein (LDL) binding with proteoglycan (PG). The me
႘	can be used for identifying compounds which disrupt LDL-PG binding
ខ្ល	without inhibiting LDL receptor binding. Such compounds can be used
႘	reduce or prevent the formation of atherosclerotic lesions and preve
႘	atherosclerosis. The transgenic non-human animals and mammals which
ပ္ပ	numan apo-B100 can be used as
ខ្ល	study of atherosclerosis, and in vivo assay methods for identifying
ပ္ပ	compounds which modulate atherosclerosis and/or LDL-PG binding. They

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Length 10, 0; Indels

DB 2; 0.028;

Score 45; Pred. No.

91.8%;

Query Match
Best Local Similarity 90.0

Sequence 10 AA;

1 TRLTRTRGLK 10 |||||||||||||| TRLTRSRGLK 10

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1; Mismatches

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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                                  Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                            Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                   100.0%; Score 49; DB 2; Length 10;
100.0%; Pred. No. 0.0044;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                       AAY30686 standard; peptide; 10 AA.
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                                                                                      Query Match
Beet Local Similarity 100.00
Beet Local Similarity 100.00
                                                                                                                                                                                                                                                                     (first entry)
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                                                                                                                                               1 TRLTRTRGLK 10
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                                                                              Sequence 10 AA;
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Homo sapiens.
                                                                                                                                                                                                                                                                       17-NOV-1999
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Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan; LDL, atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation.

Homo sapiens WO9946598-A1

Synthetic.

AAY30684 standard; peptide; 10 AA.

RESULT 3

AAY30684

(first entry)

17-NOV-1999

AAY30684;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atheroselerosels. The peptides are derived from animo acids 3358 to 3367 of apo8100. The method comportises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding withbut inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulates atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or atung composition result in an increase in a particular food or atung composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10 AA;
AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which can mainto acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo assay methods for identifying compounds which medulate atheroselerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
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Claim 17; Page 57; 70pp; English.

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing

98US-0077618P. 99WO-US004805

05-MAR-1999; 10-MAR-1998;

16-SEP-1999.

Innerarity TL, Boren JOS;

WPI; 1999-551509/46.

(REGC) UNIV CALIFORNIA

Claim 17; Page 57; 70pp; English.

atherosclerosis.

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Gaps

Synthetic.

AAY30683;

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atherosaclerosis. The peptides are derived from aminon acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDD-FG binding withbut inhibiting LDD receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDD-FG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether catherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                 Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                                                                     Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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Pred. No. 0.071;
0; Mismatches
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90.0%;
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                                                                      (first entry)
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                Homo sapiens.
                                                                      17-NOV-1999
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AAY30687
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                                                                                                                                                                                                                                                                                   Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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90.0%; Pred. No. 0.071;
tive 0; Mismatches
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                                                                                                                                        AAY30683 standard; peptide; 10 AA.
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TRLTRARGLK 10
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Best Local Similarity
Matches 9; Conserv
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Gaps

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RESULT 5
AAY30682
ID AAY3

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Length 10; 1; Indels 4

us-09-823-418-4.rag

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 septide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with caturally occurring, receptor-competent LDL particles are useful as: (i) atturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B ceptor-competent complete apo B 
                                                                                                                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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Pred. No. 0.079;
0; Mismatches
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TRLTRKRGLK 11
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Best Local Similarity
Matches 9; Conserv
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Modified-site
                                                                                        25-SEP-1997;
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Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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Pred. No. 0.071;
0; Mismatches 1; Indels
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90.0%;
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TRLTRQRGLK 10
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Best Local Similarity
Matches 9; Conserv
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                                                                                                               Homo sapiens
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RESULT 7 AAW57205

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Length 11; 1; Indels

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Matches
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                                                                                                                                                                   The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein ceceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences. RABYKOWARRH (1) or TRALYERGELK (2), or thair climers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                           Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-coagulant, apolipoprotein B-100, apoB-100, metastatic spread, thromboplastin-mediated process, cancer; inhibitor; blood coagulation, angiogenesis; cellular differentiation, apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 2; Length 13;
Pred. No. 0.093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW41261 standard; peptide; 15 AA
                                      Baillie
                                                                                                                                               Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                        87.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB001255
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                                                                                                       receptor - useful as, e.g. that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAY-1998 (first entry)
            (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
                                       Owens MD,
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TRLTRKRGLK 12
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                                                                 WPI; 1998-230637/20.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-MAY-1997;
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                                      Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW41261;
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Peptide fragments of apo: lipo: protein B-100 with anticoagulant activity

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This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). 21-KAQ-X1-KACKARKS-X2-T-22 (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 anino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent processes, specifically to prevent or reduce blood coagulation (e.g. curing or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibite activation of the prothrombinase complex; and prevents activation of cativation of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-emall cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising nucleic acid bound to LDL or VLDL lipoprotein used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW96878-97 represent nuclear localisation signal sequence derived from
used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ApoB-100 nuclear localisation signal sequence, residues 3353-3367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%; Score 43; DB 2; Length 15; 90.0%; Pred. No. 0.11; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RC, Moore JP;
                                                                        60pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW96892 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-00079030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guevara JG, Hoogeveen
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TRLTRKRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1997;
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human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumarcid arthritis, diabetic retinopathy and hypoxia. This aequence represents a heparin binding peptide relating to the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a ligand comprising of at least one sulfated or sulfonated amino
d for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                    Gaps
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0
                                                                                                                                                                                                                                  2; Length 15;
                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                 DB 2;
0.11;
                                                                                                                                                                                                                               Score 43; DB 2
Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                                        ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 2; 79pp; English.
                                                                                                                                                               fibrosis and arteriosclerosis
                                                                                                                                                                                                                            87.8%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                              9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                          1 TRLTRTRGLK 10
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TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ETHZ-) ETH ZUERICH (UYZU-) UNIV ZURICH
                                                                                                                                                                                                                                           Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                               Sequence 15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density liopprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 liopphilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKNWHRH (1) or TRAIRKRGLK (2), or their dimens. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for containing, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                 Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide binding to apo B protein delivering drugs to cancer cells
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Pred. No. 0.16;
0; Mismatches 1; Indels
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                                                                                                                                                                                    Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                      note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                    /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
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                                                                                                 AAW57208 standard; peptide; 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          97WO-GB002610.
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                                                                                                                                                          (first entry)
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Best Local Similarity 90.0
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TRLTRKRGLK 16
TRLTRTRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 TRLTRKRGLK 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 22 AA;
                                                                                                                                                                                                                                                                                                         Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                 Modified-Bite
                                                                                                                                                           03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-1997;
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                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                    AAW57208
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Gaps

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1; Indels

87.8%; Score 43; DB 6; Length 20; 90.0%; Pred. No. 0.14;

0; Mismatches

Conservative

Query Match Best Local Similarity Matches 9; Conserv

Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;

Human apoB-100 derived peptide p62.

(first entry)

17-MAY-2002

AAE14541;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-actuaring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creeptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKNKHRH (1) or THALMKRGAK (2), or their claimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles are consistent apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                        Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 22;
                                                                                                                     Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                             /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87.8%; Score 43; DB 2; 90.0%; Pred. No. 0.16; tive 0; Mismatches
                                                                                                                                                                                                                      Location/Qualifiers
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                                              AAW57209 standard; peptide; 22 AA
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                                                                                                                                                                                                                                                                                                                       97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                               96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       that express this receptor.
                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                      (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                               Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-230637/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 22 AA;
                                                                                                                                                                                                                      Key
Modified-site
                                                                                                                                                                                                                                                                                                                       25-SEP-1997;
                                                                                                                                                                                                                                                                       WO9813385-A2
                                                                                                                                                                                                                                                                                                                                               27-SEP-1996;
                                                                                             03-AUG-1998
                                                                                                                                                                                                                                                                                              02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                              Halbert GW,
                                                                                                                                                                                              Synthetic.
                                                                     AAW57209;
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New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density

18-JUL-2000; 2000GB-00017641. 18-JUL-2001; 2001WO-GB003212.

WO200206314-A2 Homo sapiens

peptide p62

24-JAN-2002

(ARKT-) ARK THERAPEUTICS LTD

WPI; 2002-179777/23

Narvanen O,

Claim 6; Page 5; 21pp; English.

lipoprotein.

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The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample autoantibodies for oxLDL in a sample, especially a serum or plasma sample cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apobl-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87.8%; Score 43; DB 5; Length 34; 90.0%; Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 TRLTRTRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 TRLTRKRGLK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
AAW96876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A MARKE KAKAKA
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Gaps ö

1; Indels

9; Conservative

Best Local Similarity Matches 9; Conserv

1 TRLTRTRGLK 10 TRLTRKRGLK 16

8

AAE14541 standard; peptide; 34 AA.

RESULT 14

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AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major aportotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (ILDL), intermediate density lipoprotein sequence can be used in the composition of the invention. The specification describes a composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                             Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense treatment.
                                                                                                                                                                                                                                           Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                              Claim 16; Fig 12C; 293pp; English
                                                                                                                                                                                                       (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                      97US-00874807.
98US-00079030.
                                                                                                                    98WO-US011927.
                                                                                                                                                                                                                                                                            WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 36 AA;
                                                                                                                                                        13-JUN-1997;
                Homo sapiens
                                                                                                                     10-JUN-1998;
                                                                                                                                                                        14-MAY-1998;
                                                  WO9856938-A1
                                                                                     17-DEC-1998
```

Search completed: December 29, 2004, 12:28:48 Job time : 61.0227 secs

ö

0; Gaps

Query Match

87.8%; Score 43; DB 2; Length 36;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 0; Mismatches 1; Indels

1 TRLTRTRGLK 10 ||||| |||| 11 TRLTRKRGLK 20

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57 ; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec е Е

US-09-823-418-4 1 TRLTRTRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	apolipoprotein B -	apolipoprotein B-1	apolipoprotein B-1	apolipoprotein B -	apolipoprotein B-1	conserved hypothet	exonuclease SpcC -	hypothetical 34.6	hypothetical prote		acetyltransferase,	apolipoprotein B-1	transcription term	hsp70 related prot	apolipoprotein B-1	probable ribosomal	hypothetical prote	probable cell surf	phosphoadenylyl-su	hypothetical prote		leucine rich repea	probable phosphopr	immediate-early pr	DNA repair protein	starch synthase (E	probable membrane	inter-alpha-trypsi	DNA-directed RNA D
SUMMAKIES	ΙD	S32802	LPHUB	C60950	JH0102	E60950	AH0906	A75337	E65112	E85985	B91140	G87383	A60950	D70375	T49646	JH0101	G71305	T16727	G95913	828609	E83363	S39854	T17033	S48288	T09313	B87455	S40051	G64921	A39967	873171
	DB	2			7										7	7	0	7		٦					7	7	7	7	7	2
	Length	965	4563	269	779	275	309	606	309	309	309	173	274	436	449	784	38	126	219	232	272	290	329	393	412	460	484	670	911	1224
	* Query Match	87.8	87.8	9.64	9.64	75.5	73.5	71.4	69.4	69.4	69.4	67.3	67.3	67.3	67.3	67.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3
	Score 1	43	43	39	39	37	36	35	34	34	34	33	33	33	33					32										
	Result No.	-	7	e	4	S	9	7	c o	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	myc-like regulator	hypothetical prote	hypothetical prote	hypothetical prote	28.9K basic DNA-bi	DNA processing pro	probable threonin	threonine dehydrat	ubiquinol-cytochro	conserved hypothet	pyruvate dehydroge	translation initia		cobyric acid synth	ferrous iron trans
A71072	T14681	T05763	E72514	T15383	A36949	D83958	A98146	AC3142	862596	B90448	DEHUPT	822579	E83061	AD3338	875294
~	N	N	N	N	~	N	~	~	N	N	н	N	~	N	-
106	146	202	208	256	260	302	304	336	339	377	388	391	412	206	614
'n.	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3	63.3
63						_	_	П	_	П	_	н	_	ч	_
31 63	31	31	31	31	31	33	m	e	m	9	m	٣	m	m	33

ALIGNMENTS

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apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 82802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: S32802
A;Accession: S32802
A;Accession: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
*Residues: 1-595 cPAP.
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301
C;Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 43; DB 2;
Pred. No. 0.81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87.8%;
90.0%;
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Gaps ö 1; Indels 0; Mismatches Query Match
Best Local Similarity 90.0
Matches 9; Conservative

226 TŘÍTŘKŘĠĽK 235 1 TRLTRTRGLK 10 a ਨੇ

apolipoprotein B-100 precursor - human

N.Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Species: Bonc-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C;Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A2 4452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc. DNA 6, 363-372, 1987

A;Title: DNA sequence of the human apolipoprotein B gene.
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Reference number: A27850; MUID:88003974; PMID:3652907
A;Accession: A27980
A;Accession: A27980
A;Accession: A27980
A;Crose-reference: UNIPROT:P01414; UNIPROT:P78492; UNIPROT:P78479; UNIPROT:Q9UMNO; UNI-R;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r. A;Reference number: A91058; MUID:87161758; PMID:3030729

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'8',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Asp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

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A; Arcestacter inturer: A9400b; MULD:B019325; FMID:35131//
A;ACCEBBIGON: A23817
A;ROCEBBIGON: A23817
A;ROCEBBIGON: A23817
A;ROCEBBIGON: A2391 cpro.
A;COSB-references: GB:M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798
A;COSB-references: GB:M12681; NID:9178797; PIDN:AAA51753.1; PID:9178798
B;Deeb, S.S.; Motulaky, A.G.; Albers, J.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 4883-4886, 1988
A;Rocession: A25774; MUD:85270450; PMID:3860836
A;Rocession: A25774; MUD:85270450; PMID:3860836
A;Rocession: A25774; MUD:85270450; PMID:3860836
A;Rocession: A25774; MUD:871918921; PIDN:AAA51759.1; PID:9178822
A;CosB-references: GB:RO3175; NID:9178821; PIDN:AAA51759.1; PID:9178822
A;CosB-references: GB:RO3175; NID:917999; PMID:2883086
A;Attle: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg
A;Accession: A25533
A;Molecule type: mRNA
A;Accession: A25533
A;Molecule type: MRNA
A;CosB-references: GB:M15421; NID:917891; PIDN:3338-3948, 'P',3950-3963,'Y',3965-4180,
A;Accession: A25573
A;Accession: A25571
A;Accession: A25571
A;Accession: A25571
A;Accession: A25671
A;CosB-references: GB:M17367; NID:9178731; PIDN:AAAS17811; PID:9178732
A;Title: Complete cDNA and derived protein sequence of human apolipoprotein B-100.
A;Reference number: A93639; MUID:87016385; PMID:3763409
A;Accession: A55263
A;Molecule type: mRNA
A;Residues: 1-272, NV.,204-617, A, 619-1217, E, 1219-2091, VV, 2093-2364, T, 2366-2679, Q, A;Residues: 1-272, NV.,214-617, A, Grant, S.M.; Higuchi, K.; Hospattankar, A; Lackner, K.; Lee, N.; Brewer Jr Proc. Natl. Acad. Sci. U. S.A. 83, 8142-8146, 1986
A;Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino A;Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 485-617, 'A', 619-1044 <LA2>
A; Cross-references: GB:M12480; NID:g178791; PIDN:AAAS1751.1; PID:g178792
R; Protter, A.A.; Hardman, D.A., Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; MUID:86149325; PMID:3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-617, 'A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N',
4189-4220, 'M', 4222-4563 c.LMA
A; Note: 1-6200. Side to the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID:8708488; PMID:3759943
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Rightlagers, C.C.; Warran, N. B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Alferonciarcule 8, 277-289, 1985
A.715te Rollerd Colning of human LDL apolytotesin B CDNa. Evidence for more than on Accessing Manner, Monday (MID18513085) PMID184481
A.Mocessuc manner, 190044 (MID18513085) PMID184481
A.Mocessuc manner, 190049 (MID1851085) PMID1804665
A.Mocessuc manner, 190049 (MID18707084) PMID1804665
A.Mocessuc manner, 190049 (MID18707084) PMID1804665
A.Mocessuc manner, 190049 (MID18707084) PMID1802716
A.Mocessuc manner, 190049 (MID18707084) PMID1802716
A.Mocessuc MID1864 (MID187084) MID1802716
A.Mocessuc MID18704 MID187084 MID1802716
A.Mocessuc MID18704 M
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applipoprotein B - golden hamster (fragment)

C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Accession: JH0102
E;Smith, T.J.
submitted to GenBank, June 1990
A;Accession: JH0102
A;Accession: JH0101
A;Accession: JH0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Gene: apoB
C,Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8; Conservative
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642 SRLTRKRGLK 651
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C, Genetics:
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A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su FrESS Lett. 170, 105-106, 1984
A;Titcle: Human apolipoprotein B: partial amino acid sequence.
A;Titcle: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID: 84208786; PMID: 6373369
A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-892, Kf, 894-896 <LE1>A;Accession: B22006
A;Molecule type: protein
A;Residues: 873-922, Kf, 894-896 <LE1>A;Accession: B22006
A;Molecule type: protein
A;Residues: 873-82006
A;Residues: 873-8006
A;Residues: 873-800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               apolygorotein B-100 - golden hamster (fragment)
C,Species: Mesocricetus auratus (golden hamster)
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C,Accession: C60950
R,Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A,Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A,Reference number: A60950; MUID: 90324804; PMID: 2373961
A,Recession: C60950
A,Molecule type: DNA
A,Residues: 11269 < LAW>
A,Residues: 11269 < LAW>
A,Residues: 1269 < LAW>
A,Coss-references: UNIPROT: Q60537; UNIPROT: Q60536
C,Superfamily: apolipoprotein B
C,Superfamily: apolipoprotein B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 269
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Pred. No. 2.5;
1; Mismatches
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Best Local Similarity 80.0%;
Matches 8; Conservative
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216 SRLTRKRGLK 225
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Best Local Similarity
Matches 9; Conserv
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C;Keywords: atherosclerosts; calcium; cholesterol metabolism; chylomicron; glycoprotein, F;435-445/Region: receptor binding F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rilaw, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A;Titlei Res. 31, 1109-1120, 1990
A;Title A cross-species comparison of the apolipoprotein B domain that binds to the LDF A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-275 <LAW>
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Darecise has also been called Salmonella typhi C;Davezoni A;Davani G;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Parrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                           Length 779;
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Pred. No. 6.4;
                                                                                                                                                           Score 39; DB 2;
Pred. No. 6.9;
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Pred. No. 30; L; Mismatches

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70.0%;
    Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                    170 rocakokcik 179
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                                                                1 TRLTRTRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <STO>
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Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: AH0906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cyaccession: A75337

Rywhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mg
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
ArTitle: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: A75337
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-909 <WHIS
A;Cross-references: UNIPROT:09R144; GB:AE002032; GB:AE000513; NID:g6459715; PIDN:AAF1147
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: AH0906
A;Status: prefidinary
A;Molecule type: DNA
A;Residues: 1-309 <PAR>
A;Residues: 1-309 <PAR>
A;Coser-references: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
C;Genetics:
A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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                                                                                                                                                                                                                   Length 309,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.4%; Score 34; DB 1; Length 309;
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                                                                                                                                                                                                                                                                                                                                                                                                                         exonuclease SbcC - Deinococcus radiodurans (strain R1)
                                                                                                                                                                                                            73.5%; Score 36; DB 2;
70.0%; Pred. No. 12;
tive 1; Mismatches 2
                                                                                                                                                                                          Query Match
Best Local Similarity 70.07
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                                                                                                                                                                                                                                                                                                                             170 TRIARERGLK 179
                                                                                                                                                                                                                                                                                         1 TRLTRTRGLK 10
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86 RVTRTRGRK 94
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A; Gene: DR1922
A; Map position: 1
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hypothetical protein yhcc [imported] - Escherichia coli (strain O157:H7, substrain EDL93. C;Species: Escherichia coli (cjate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: EB5985 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, aller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P45476; GB:AE005174; NID:g12517812; PIDN:AAG58345.1; G3PDB:G.A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1.309 <HAY>
A;Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:G
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: yhcC
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
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69.4%; Score 34; DB 2;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches
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Gaps

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Length 436 1; Indels

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C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49646
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
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Ligid Res. 31, 1109-1120, 1990
A.Titleid Res. 31, 1109-1120, 1990
A.Titlei A cross-species comparison of the apolipoprotein B domain that binds to the LD
A.Reference number: A60950; MUID:90324804; PMID:2373961
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C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           apolipoprotein B-100 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Cate: 17-Apr.-1993 #sequence revision 17-Apr.-1993 #text_change 09-Jul-2004
C;Cate: 17-Apr.-1993 #sequence revision 17-Apr.-1993 #text_change 09-Jul-2004
C;Accession: JH0101; S33128; D60950
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-J10, 1990
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of A;Reference number: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9P584; ЕМВL:AL355932; GSPDB:GN00116; NCSP:B5O22.280
A;Experimental source: BAC clone B5O22; strain OR74A
                                                                                                                                                                                                                                                                                                                                         - Neurospora crassa
         DB 2;
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                                     Pred. No. 66;
0; Mismatches
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A;Residues: 1-784 <SMI>
A;Cross-references: UNIPROT:Q61314; GB:M35186
A;Smith, T.; Hautamaa, D.; Maeda, N.
submitted to the EMBL Data Library, May 1989
      Score 33;
Pred. No. 6
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A;Residues: 427-531,'S',533-700 <LAW>
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A,Accession: S33128
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-531, 'S',533-784 <SM2>
A,Crosg-references: EMBL:X15191
      67.3%;
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                                                                                                                                                                                                                                                                                                                                         hsp70 related protein [imported]
                                     Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 6
A;Introns: 87/1; 161/2; 339/3
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404 TRLTTTKGVE 413
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Rivierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J. R.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. J.; Title: Complete Genome Sequence of Caulobacter crescentus.
A;Recession: G87383
A;Recession: G87383
A;Satus: preliminary
A;Residues: 1-173 cSTO>
A;Residues: 1-173 cSTO>
A;Cross-references: UNIPROT: Q949B1; GB: AE005673; NID: g13422385; PIDN: AAX23067.1; GSPDB: C;Genetics:
A;Gene: CC1083
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Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:9819666; PMID:9537320

A;Accession: D70375

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Residues: 1-436 <AQP:
A;Cross-references: UNIPROT:067031; GB:AE000711; NID:g2983401; PIDN:AAC06989.1; PID:g298

A;Experimental source: strain VF5

C;Genetics:
A;Gene: Tho

C;Superfamily: transcription termination factor rho

C;Keywords: transcription termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A.Title: A cross species comparison of the apolipoprotein B domain that binds to the LDI A; Reference number: A60950; MUID:90324804; PMID:2373961
A; Reference number: A60950; MUID:90324804; PMID:2373961
A; Accession: A60950
A; Molecule type: mRNA
A; Residues: 1-274 < LAN>
A; Cross-references: UNTRROT:Q7M2U9
A; Note: authors translated the codon GAT for residue 155 as His
C; Superfamily: apolipoprotein B
C; Superfamily: apolipoprotein B
C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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C;Species: Aquifex aeolicus
C;Date: OB-May-1998 #sequence_revision O8-May-1998 #text_change O9-Jul-2004
C;Accession: D70375
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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C;Species: Oryccolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A60550
R;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
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ilarity 77.8%;
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0; Gaps Query Match 67.3%; Score 33; DB 2; Length 784; Best Local Similarity 70.0%; Pred. No. 1.2e+02; Matches 7; Conservative 1; Mismatches 2; Indels

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Search completed: December 29, 2004, 12:39:02 Job time : 10.6591 secs

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus. NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

MEDLINES-22761261; PubMed=12878460;

Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

MOI. Phylogenet. Evol. 28.225-240(2003).

EMBL; AFS48396; AAP97352.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apolipoprotein B (Fragment).
Macaca feasticularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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TISSUB-Liver;
TISSUB-201708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Length 414;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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             Q7ZET5
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Q7Z405
Q7TN63
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Q7R4X6
Q7R4X6
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Name=apoB-100,
Aotus vociferans (Spix's owl monkey).
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RESULT 3

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Mammalia; Butheria; Primates; Catarrhini; Hominidae, Homo
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Nucleic Acids Res. 13:8813-8826(1985).
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MEDLINE=85270450; PubMed=3860836;
Deeb S.S., Motullary A.G., Alberra, J.J.;
"A partial cDNA clone for human apolipoprotein B.
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985).
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                      NCBI_TaxID=9606;
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MEDLINE-87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiena (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
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Last annotation update)
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GO:0005319; F:lipid transporter activity; NAS.
GO:0006869; P:lipid transport; NAS.
TER
                                                                                                                                                                                                 Score 43; DB 2;
Pred. No. 2.7;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                               PRT; 3262 AA.
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Pred. No. 18;
0; Mismatches
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the B-74 region.";
Gene 49:29-51(1986).
EMBL; M15421; AAA51758.1; -.
PIR; A27850; LPHUB.
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Best Local Similarity 90.00,
Best Local 9; Conservative
                                                                                                      EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                                                                                                                                                             9; Conservative
                                                                TISSUE=Liver;
Murray R.;
Submitted (FEB-1992) to
                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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Name=APOB;
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596
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SEQUENCE FROM N.A.
MEDIJINE=87016385; PubMed=3763409;
KEDOLT T.C., Walls S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolloporotein B-"The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986). MEDLINE=85300528; PubMed=294225; Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S., Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M., Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B., Mahley R.W., Scott J.; "Human apolipoprotein B: structure of carboxyl-terminal domains, sites of gene expression, and chromosomal localization."; Science 230:37-43(1985). [3]
SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE-87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Ur., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-SEQUENCE OF 3056-3159 FROM N.A.
MEDIATR=866041888; PubMed=3903660;
Medrablan M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgessner T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.;
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characterization of mRNA." [8] SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181. MEDLINE-86093680; PubMed=3841204; Carlsson P., Olofeson S.O., Bondjers G., Darnfors C., Wiklund O., Bjursell G.; SEĞUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; Pubmed-3652907;
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Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
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DNA 6:363-372(1987). SEQUENCE FROM N.A. MEDLINE=87161758; PubMed=3030729; Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D., Zannis V.I.;

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VARIANT LEU-2739.
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Proter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V.,
Chen G.C., Kircher S.W., McEnroe G., Kane J.P.;
"Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
Nature 323:738-742(1986).
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Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cal S.-J., Deslypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.,
"Applipoprotein B-48 is the product of a messenger RNA with an organ-
                                                                                                                                                                                                                                                                                                                                                 MEDLINE 97039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
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MEDLINE=86287319, PubMed=3861454,
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M. Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B.";
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Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.;
"Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene.";
Hum. Genet. 86:91-93(1990).
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MEDLINE-89098975; PubMed-2563166;
Soria L.F., Ludwig B.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
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MEDLINE=20143590; PubMed=10679026;
Shao Y., McCabe J.B., Vance J., Berthiaume L.G.;
"Palmitoylation of apolipoprotein B is required for proper intracellular sorting and transport of cholesteroyl esters and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=86242245; PubMed=3087360;
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                                                                apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                 PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
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Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G.,
Krempf M., Girandet P., Junien C., Boilau C.,
"Familial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500--SGLN and ARG3531-->CYS mutations in a French
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-1- FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
-1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                        MEDLINE=55190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Prost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
Mendel C.M., Prost P.H., Papolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
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Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
                                                                  gene at position 8344.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDIATE-9911125; PubMed-9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C., Ahearn M.O., Kuldanek S.A., Rajkumar N., Toth B.J., Yi Q., Nickerson D.A.; dullanek S.B. BMBL/GenBank/DDBJ databases.
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Ag(X) antigen).
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Pred. No. 26;
MEDLINE=91016974; PubMed=2216805;
Huang L.-S., Gavish D., Breslow J.L.;
"Sequence polymorphism in the human apoB
Nucleic Acids Res. 18:5922-5922[1990].
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MEDLINE-97403938; PubMed-9259199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97044521; PubMed=8889592;
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Hum. Genet. 102:44-49
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Mol. Phylogenet. Evol. 28:22
EMBL; AY243375; AAP50763.1;
                                                                                                 Local Similarity 80.0
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Les 8; Conservative
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279 SRLTRKRGLK 288
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436 4.
436 AA;
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                                Lipoprotein.
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SEQUENCE 432
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Q7YQM8
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4polipoprotein B (Fragment).
Glaucomys volans (Southern flying squirrel).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Petauristinae;
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MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AY243379; AAP50767.1;
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MEDLINBE-22761261; PubWed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
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Mammalia, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
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                                                                                                                               Length 4563;
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                                                                                                     4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                     Indels
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EMBL; AY324608; AAP72970.1; -. GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:0005869; P:lipid transport; IEA. InterPro; IPR009454; DUF1081.
InterPro; IPR001747; Lipid_transport_N. Pfam; PF06448; DUF1081; 1. SMART; SM00538; LPD_N; 1.
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Biceros bicornis (Black rhinoceros).
                                                                                                                                                                                                                                                       421 AA
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Pred. No. 26;
0; Mismatches
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                                                                                                                            87.8%;
                                                                                                                                                  9; Conservative
                                                                                                                                                                                     3385 TRLTRKRGLK 3394
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264 SRLTRKRGLK 273
                                                                                                                                                                       1 TRLTRTRGLK 10
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                                                                                                                          Query Match
Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lipoprotein.
NON TER
NON TER 42
                                                                                           Lipoprotein.
SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                                     Glaucomys.
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Matches
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Gaps
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Nyctimene.
NCBI_TaxID=48988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
Amsw phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
MOI. Phylogenet. Evol. 28:225-240(2003).
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MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261; R.-P., Wayne R.K., Springer M.S.;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
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                                                                                                                                                                                              Score 39; DB 2; Length 432;
Pred. No. 14;
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                                                                                                         432 A3; 48171 MW; F27B7AB39604732C CRC64;
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48717 MW; 1C4A7EAD72D2C629 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
Name=apoB-100,
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28:225-240(2003)
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Gaps
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Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships ";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apolipoprotein B (Fragment).
Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Hydrochaeridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; MY2431369; AAP50757-11;
InterPro; IPRO00871; Beta lactamase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                              Agouti paca (Paca).
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
NCBI_TaxID=108852;
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                                 79.6%; Score 39; DB 2; Length 445; llarity 80.0%; Pred. No. 14; Conservative 1; Mismatches 1; Indels
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445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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                                                                                                                                            288 SRLTRKRGLK 297
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                                                                                                        1 TRLTRTRGLK 10
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              Query Match
Best Local Similarity
Laca 8; Conserve
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                                                                                                                                                                                                                                                                                                                                               Name=apoB-100;
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NON TER 44
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NON TER 4
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 SEQUENCE
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Matches
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Frament).
Rousettus amplexicaudatus (Common rousette).
Rousettus amplexicaudatus (Common rousette).
Rousettus Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Bvol. 28:225-240(2003).
EMBL; AY243383; AAP50771.1;
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MEDLINE-2761261, bubMed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";

MOI. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAP50766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chaetophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Edentata, Dasypodidae, Chaetophractus.
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                                                                                                        Length 438;
                                                                                                                                            1; Indels
                                                                     48734 MW; 2BD85BCBF4E2CC41 CRC64;
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1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                     Score 39; DB 2;
Pred. No. 14;
1; Mismatches
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                                                                                                        79.6%;
EMBL; AF548436; AAP97392.1;
                                                                                    Ouery Match
Best Local Similarity 80.v.
8; Conservative
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438 AA; 4REC
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Best Local Similarity 80.0
Matches 8; Conservative
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281 SRLTRKRGLK 290
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                                                                     438 AA;
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445
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SEQUENCE 43
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MEDLINE=90236327; PubMed=2332175;
MEDLINE=90236327; PubMed=2332175;
MEDLINE=90236327; PubMed=2332175;
Maeda N.;
"Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";
EMBL, M35187; AAA37059.1; -.
PIR; JH0102; JH0102.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment)
Exethizon dorsatum (North American porcupine)
Exethizon Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Marine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
10-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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              Score 39; DB 2; Length 445; Pred. No. 14;
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NON_TER 445
SEQÜENCE 445 AA; 49617 MW; 9572FESF5E7625F2 CRC64;
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780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
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                                                                 1; Mismatches
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        79.6%;
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Best Local Similarity 80.00,
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288 SRLTRKRGLK 297
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                                                                                                            1 TRLTRTRGLK 10
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288 SRLTRKRGLK 297
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Query Match
Best Local Similarity
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78
SEQUENCE 78
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Query Match
79.6%; Score 39; DB 2; Length 780;
Best Local Similarity 80.0%; Pred. No. 27;
Matches 8; Conservative 1; Mismatches 1; Indels
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Search completed: December 29, 2004, 12:37:31 Job time : 59.5202 Becs

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December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Database

		Description		Aay30686 Apo-B100	- 1	-	•				Aaw57207 Apo B 100	Aaw41261 Apolipopr		Abj37575 Heparin b	Apo	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo	Aaw96845 Nucleic a	Abb37687 Peptide #	Abg52504 Human liv	Aar72704 Human apo		Adj57400 Human apo		Aaw41262 Apolipopr	Aaw96826 Amino aci
SUMMARIES		ID		AAY30686	AAY30684	AAY30685	AAY30683	AAY30682	AAY30687	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826
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ALIGNMENTS

Apo-B100; proteoglycan receptor mutation, atherosclerosis; low density lipoprotein; proteoglycan; LDL, atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. AAY30686 standard; peptide; 10 AA. Claim 17; Page 57; 70pp; English. 98US-0077618P. 99WO-US004805. Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Synthetic. Homo sapiens. W09946598-A1 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999. AAY30686; AAY30666

AAY306666

AAY306666 RESULT 1

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate artherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which strengs and in vivo models system for the study of atherosclerosis, and in vivo models system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can

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Sequence 10 AA;

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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                               Gaps
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                                                    100.0%; Score 48; DB 2; Length 10; 100.0%; Pred. No. 0.0073; .ive 0; Mismatches 0; Indels
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compounds the method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atheriation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the able to be used to identify compounds which result in an increase in also be used in gene therosclerotic lesions. The polymucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
Claim 17; Page 57; 70pp; English.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which aredeptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from animo acids 3358 to 3367 of apoB100. The method comportises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent catheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used an in vivo model system for the compounds which modulate atheroselerosis and/or LDL-PG binding. They can compounds which modulate atheroselerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether can particular food or drug composition tends to stimulate or inhibit the formation of atheroselerotic lesions. The polynuclectides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method compounds witch affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent catherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether atherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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Apo-B100 derived peptide showing a proteoglycan receptor mutation.

AAY30682 standard; peptide; 10 AA.

RESULT 5 AAY30682 ID AAY3

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25-SEP-1997;

02-APR-1998

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Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                               AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect can be used for identifying compounds which affect without inhibiting LDL receptor binding which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which etudy of atheroselerosis, and in vivo assay methods for identifying compounds which medulate atheroselerosis and/or LDL-PG binding. They can study of atheroselerosis, and in vivo assay methods for identifying compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the contact of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.7%; Score 44; DB 2; Length 10; 90.0%; Pred. No. 0.047; 1; Indels :ive 0; Mismatches 1; Indels
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ID AAW57205 standard; peptide; 11 AA.
Claim 17; Page 57; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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WO9813385-A2

Synthetic

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media sepecially as growth supplements. Non-naturally occurring, creceptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 44; DB 2;
Pred. No. 0.052;
0; Mismatches
                                                                                                                                         Baillie G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                 Claim 12; Page 52; 73pp; English.
                                                                           96GB-00020153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%;
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                                                                                                          (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Conservative
                                                                                                                                       Halbert GW, Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TRLTRSRGLK 10
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TRLTRKRGLK
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                                                                           27-SEP-1996;
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-actually occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KARYKKNKHRH (1) or THALTRERGIK (2), or their claimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for call culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles are apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity
                                                                                                                  Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-coagulant, apolipoprotein B-100, apoB-100, metastatic spread, thromboplastin-mediated process, cancer; inhibitor; blood coagulation, angiogenesis; cellular differentiation; apoptosis; KRAD-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 13;
Pred. No. 0.062;
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                                                 Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.7%;
90.0%;
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                                                                                                                                                       that express this receptor.
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                 (UYST ) UNIV STRATHCLYDE.
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                                                   Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TRLTRSRGLK 10
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                                                                                   WPI; 1998-230637/20.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9743311-A1
                                                 Halbert GW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-NOV-1997.
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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apol-100). IL-KAO-XL-KRNKHRHS-X2-T-Z2 (I) XI = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide, or terminal amide group or 1-77 a. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent containing the peptide are used for simultaneous, concesses, specifically to prevent or reduce blood coagulation (e.g. during or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits or activation of the prothrombinase complex; and prevents activation of actor VII on the surface of thromboplastin and of platelets by thrombin.
                                                                                                                                                                                                                                                                                                                                                       It binds to the residues 58-66 of thromboplastin and of platelets by thrombin. smaller than apoB-100, they act more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollyoprotein; blidding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW96878-97 represent nuclear localisation signal sequence derived from
used for treating or preventing coagulation, inhibiting anglogenesis, cell differentiation and apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%; Score 44; DB 2; Length 15; 90.0%; Pred. No. 0.071; 1ive 0; Mismatches 1; Indels
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                                                         60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW96892 standard; peptide; 15 AA.
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TRLTRKRGLK 10
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                                                         Disclosure; Page 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15 AA;
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TRLTRSRGLK 10 7 TRLTRKRGLK 16

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human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         ABJ37575 standard; peptide; 20 AA.
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                                                                                                                                                                             fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                  91.7%;
90.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                    9; Conservative
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TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                   1 TRLTRSRGLK 10
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                Sequence 15 AA;
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(UYZU-)
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Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.

'note= "attached to retinoic acid" /note= "attached to cholesterol"

Location/Qualifiers

Key Modified-site Modified-site

Synthetic.

Apo B 100 binding site peptide analogue peptide C.

(first entry)

AAW57208 standard; peptide; 22 AA.

RESULT 12 AAW57208

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AAW57208;

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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKNWHRH (1) or TRLTRKRGLK (2), or their dimention are peptides containing, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 44; DB 2;
Pred. No. 0.11;
0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRLTRSRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 9; Conserv
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Gaps

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1; Indels

91.7%; Score 44; DB 6; Length 20; larity 90.0%; Pred. No. 0.096; Conservative 0; Mismatches 1; Indels

Query Match Best Local Similarity Matches 9; Conserv

Sequence 20 AA,

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Baillie G;

Owens MD,

Halbert GW,

WPI; 1998-230637/20.

(UYST) UNIV STRATHCLYDE.

97WO-GB002610. 96GB-00020153

25-SEP-1997;

02-APR-1998.

27-SEP-1996;

WO9813385-A2

(first entry)

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New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to peptides having affinity for oxidised low density lipoprotein (OxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for OxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's blood, and has a long half-life. The present sequence is human apos-100 derived peptide p62 used in the invention
                                                                                                     Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                      Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                 18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                             18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                   (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-179777/23
                                                                                                                                                                                                                                  WO200206314-A2.
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                              peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                       Narvanen O,
                                  17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoprotein.
                                                                                                                                                                                                                                                                        24-JAN-2002
AAE14541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein creceptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKKNKHH (1) or TTRIFKRGLK (2), or their consect Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding effinity to an apo B protein receptor
                                                                                                                                                                                                             Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 2; Length 22;
                                                                                                                                                                                                                                                                                                                                                                /note= "attached to retinoic acid"
                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Owens MD, Baillie G;
                                                                    AAW57209 standard; peptide; 22 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97WO-GB002610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96GB-00020153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                that express this receptor.
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYST ) UNIV STRATHCLYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-230637/20
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                              Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                    WO9813385-A2
                                                                                                                                         03-AUG-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Halbert GW,
                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                      AAW57209;
                                  RESULT 13
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Yla-Herttuala S

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                                                                                                                                                                                                                                                                                                                     Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                           Gaps
                                                           ;
0
                                                                                                                                                                                                                                                                                          Nucleic acid binding domain from apoB-100, residues 3348-3390.
                         Score 44; DB 5; Length 34; Pred. No. 0.17;
                                                         1; Indels
                                                           0; Mismatches
                                                                                                                                                                                                  AAW96876 standard; peptide; 36 AA.
                         91.7%;
90.0%;
                                                                                                                                                                                                                                                             22-APR-1999 (first entry)
                                         Best Local Similarity 90.0
Matches 9; Conservative
                                                                                        1 TRLTRSRGLK 10
                                                                                                                     34
                                                                                                                25 TRLTRKRGLK
Sequence 34 AA;
                                                                                                                                                                                                                                AAW96876;
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Gaps

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1; Indels

9; Conservative 1 TRLTRSRGLK 10

Matches

8 g

16

TRLTRKRGLK

AAE14541 standard; peptide; 34 AA.

RESULT 14 AAE14541 ID AAE1 XX

Homo sapiens

WO9856938-A1 17-DEC-1998.

97US-00874807. 98US-00079030. 98WO-US011927

10-JUN-1998; 13-JUN-1997; 14-MAY-1998;

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AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major aportotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (ILDL) and lipoprotein a The present sequence can be used in the composition of the invention. The present apportation factor and escribes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                         Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                       Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                Claim 16; Fig 12C; 293pp; English.
                                                                                                                                                                                                             (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                         WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                               treatment.
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Search completed: December 29, 2004, 12:28:48 Job time : 61.0227 secs 11 TRLTRKGLK 20 g

1 TRLTRSRGLK 10

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Gaps ;

Query Match
91.7%; Score 44; DB 2; Length 36;
Best Local Similarity 90.0%; Pred. No. 0.18;
Matches 9; Conservative 0; Mismatches 1; Indels

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91.7%;
90.0%;
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Best Local Similarity 90.vv,
9; Conservative
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SOFTWARE: Patentin Ver. 2.1
3382 řŘLŤŘKŘĠĽK 3391
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ORGANISM: Homo sapiens
LENGTH: 4560
                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-398-200-2
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 SEQ ID NO 2
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Sequence 25, Appl
Sequence 72046, A
Sequence 5628, Ap
Sequence 5939, Ap
Sequence 576, Appl
Sequence 70, Appl
Sequence 8115, Ap
Sequence 8115, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 73828, p. Sequence 42481, p. Sequence 5564, p. Sequence 13596, p. Sequence 11685, p. Sequence 11686, p. Sequence 11687, p. Sequence 116887, p. Sequence 11687, p. Sequence 1168
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69335,
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73828,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                             December 29, 2004, 12:28:58 ; Search time 8.97727 Seconds (without alignments) 51.960 Million cell updates/sec
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Sequence 6
Sequence 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
8: /cgn2_6/ptodata/2/paa/US11_NEW_COMB.pep:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-868-577A-25
US-11-001-793-5628
US-11-001-793-5939
US-11-001-793-5939
US-11-001-793-5939
US-10-90-3513-70
US-10-990-328-8115
US-10-990-328-8115
US-10-990-328-8115
US-10-990-328-8115
US-10-990-328-8115
US-10-910-891-167
PCT-USO2-09107B-52732
PCT-USO2-09107B-52732
PCT-USO2-09107B-52732
PCT-USO2-09107B-51874
PCT-USO2-09107B-51878
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US-10-990-328-11686
US-10-990-328-11687
US-10-990-328-11688
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                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          187395 segs, 46645940 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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48
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Match Length DB
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5535
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Result Š.

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Sequence 14, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 2245, A
Sequence 30, Appl
Sequence 561, Appl
Sequence 561, Appl
Sequence 1915, Appl
Sequence 6931, Appl
Sequence 6931, Appl
Sequence 540, Appl
Sequence 540, Appl
Sequence 2841, Appl
Sequence 77577, Appl
Sequence 77577, Appl
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Seq
                                        US-10-511-989-14
US-10-511-989-12
PCT-USO4 31832-4
US-10-983-340-4
US-10-220-366A-2245
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US-10-399-1393-0
US-10-408-765-840
US-10-408-765-1915
US-10-408-765-1918
PCT-USO2-09107B-6931
PCT-USO2-09107B-65307
US-10-408-765-2841
PCT-USO2-09107B-45399
PCT-USO2-09107B-45979
PCT-US02-09107B-66243
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ALIGNMENTS

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TITLE OF INVENTION: METHOD OF INHIBITING INFECTION BY HCV, OTHER TITLE OF INVENTION: METHOD OF INHIBITING INFECTION BY HCV, OTHER TITLE OF INVENTION: PLANIVIRIDAE VIRUSES, AND ANY OTHER VIRUS THAT TITLE OF INVENTION: COMPLEXES TO LOW DENSITY LIPOPROTEIN OR TO VERY LOW TITLE OF INVENTION: INTO A CELL TITLE OF INVENTION: INTO A CELL TITLE OF INVENTION: INTO A CELL CITLE OF INVENTION INDOMER: US/10/398,200
CURRENT FILING DATE: 2003-104-03
PRIOR PILLING DATE: 2000-10-25
PRIOR FILING DATE: 2000-10-25
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Pred. No. 3;
0; Mismatches 1; Indels
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TITLE OF INVENTION: HEPARIN BINDING VEGFR-3 LIGANDS
FILE REFERENCE: 28967/39359A
CURRENT APPLICATION NUMBER: US/10/868,577A
CURRENT FILING DATE: 2004-06-14
PRIOR APPLICATION NUMBER: US 60/478,390
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-06-12
PRIOR FILING DATE: 2003-09-23
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-868-577A-25; Sequence 25, Application US/10868577A; GENERAL INFORMATION:
; Sequence 2, Application US/10398200
; GENERAL INFORMATION:
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FEATURE:

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PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR FILING DATE: 1997-05-23
PRIOR PLICATION NUMBER: US 60/056,845
PRIOR PLIING DATE: 1997-08-22
PRIOR PLIING DATE: 1997-08-22
PRIOR PLLING DATE: 1997-06-21
PRIOR PLLING DATE: 1997-04-11
PRIOR PLLING DATE: 1997-05-23
PRIOR PLLING DATE: 1997-05-23
PRIOR PLLING DATE: 1997-08-22
PRIOR PLLING DATE: 1997-04-11
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GENERAL INFORMATION:

JAPPLICANT: Rosen, et al.

TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: P8900

CURRENT PILING DATE: 2004-12-02

PRIOR APPLICATION NUMBER: US/11/001,793

CURRENT FILING DATE: 1997-03-07

PRIOR PILING DATE: 1997-03-07

PRIOR PILING DATE: 1997-04-11

PRIOR PILING DATE: 1997-04-11

PRIOR PILING DATE: 1997-04-11

PRIOR PPLICATION NUMBER: US 60/040,162

PRIOR PILING DATE: 1997-04-13

PRIOR PILING DATE: 1997-04-11

PRIOR PILING DATE: 1997-05-23

PRIOR PILING DATE: 1997-04-11

PRIOR PILING DATE: 1997-05-23

PRIOR PILING PAPEL CATION NUMBER: US 60/047, 632

PRIOR PILING DATE: 1997-05-23

PRIOR PILING DATE: 1997-05-23

PRIOR PILING DATE: 1997-05-23

PRIOR PILING PAPEL SPACENTIN VET: 2.0

SOFTWARE: PARENTIN VET: 2.0

SOFTWARE: PARENTIN VET: 2.0
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Pred. No. 48;
0; Mismatches 1; Indels
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Pred. No. 5.9;
0; Mismatches 1; Indels
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87.5%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-11-001-793-5628
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US-11-001-793-5939
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GENERAL INFORMATION:
APPLICAMTON:
APPLICAMTON:
ITILE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034VPC
CURRENT APPLICATION NUMBER: PCT/US02/09107B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/946,993
PRIOR FILING DATE: 2001-09-06
PRIOR APPLICATION NUMBER: 06/942,923
PRIOR PILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 06/342,923
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 06/342,923
PRIOR FILING DATE: 2001-02-06
PRIOR PLING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 06/362,699
PRIOR PLING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 78614
SEQ ID NO 72046
LENGTH: 289
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Sequence 5628, Application US/11001793

GENERAL INFORMATION:

APPLICANT: ROSEN, et al.

TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS90

CURRENT APPLICATION NUMBER: US/11/001,793

CURRENT APPLICATION NUMBER: US/10/100,683

PRIOR PILING DATE: 2002-03-19

PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: US 60/040,162

PRIOR FILING DATE: 1997-03-07

PRIOR APPLICATION NUMBER: US 60/043,576
                                                                                                                                        NAME/KEY: misc feature
LOCATION: (32) ... (126)
OTHER INFORMATION: heparin binding domain
                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature

// LOCATION: (3161).. (3236)

// OTHER INFORMATION: heparin binding domain

US-10-868-577A-25
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                                   TYPE: PRT
ORGANISM: Homo sapiens
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Matches 8; Conserv
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TITLE OF INVENTION: Methods and Compositions for the Introduction of Polynucleotides FILE REFERENCE: 120701-2030
CURRENT APPLICATION NUMBER: 08/10/972,963
CURRENT FILING DATE: 2004-10-25
PRIOR APPLICATION NUMBER: 60/568,436
PRIOR FILING DATE: 2004-6-05
PRIOR FILING DATE: 2003-10-24
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PATENT OF SEQ ID NOS: 218
SOFTWARE: PATENT OF SEQ ID NOS: 218
SOFTWARE: PATENT OF SEQ ID NOS: 218
LENGTH: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: CARGILL, Michele
TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001495
CURRENT APPLICATION NUMBER: US/10/990,328
CURRENT FILING DATE: 2004-11-17
NUMBER OF SEQ ID NOS: 558024
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8115
LENGTH: 441
TYPE: PRI
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US-10-990-328-8116

US-10-990-328-8116

Sequence 8116, Application US/10990328

Sequence 8116, Application US/10990328

Sequence 8116, Application US/10990328

TOTHER OF INVENTION: DOLYMORPHISMS IN NUCLEIC ACID MOLECULES

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

TITLE OF INVENTION: USES THEREOF

CURRENT APPLICATION NUMBER: US/10/990,328

CURRENT APPLICATION NUMBER: US/10/990,328

CURRENT APPLICATION NUMBER: US/10/990,328

SOUTHARD OF SEQ ID NOS: 558824

SOUTHARD OF SEQ ID NOS: 558824

SEQ ID NO 8116

LENGTH: 441
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Pred. No. 63;
1; Mismatches
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70.0%;
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Best Local Similarity 70.0.
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Best Local Similarity 70.0
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
US-10-972-963-70
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US-10-990-328-8115
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US-10-990-328-8116
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US-10-990-328-8115
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GENERAL INFORMATION:
APPLICANT: Gencia Corporation
APPLICANT: Khan, Shaharyar
TIPLICANT: Khan, Shaharyar
TIPLICANT: Khan, Shaharyar
TIPLICANT: The Corporation of Polymucleotides
FILE REFERENCE: 120701-2030
CURRENT APPLICATION NUMBER: PCT/US04/35137
CURRENT APPLICATION NUMBER: 60/568,436
PRIOR FILING DATE: 2004-11-03
PRIOR FILING DATE: 2004-10-24
NUMBER OF SEQ ID NOS: 218
SOFTWARE: PatentIn version 3.3
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SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta SEQ ID NO 576
LENGTH: 309
                                                                                                                                                 Sequence 576, Application US/10482526A
GENERAL INFORMATION:
APPLICANT: Syngenta Participations AG
TITLE OF UNURATION:
CURRENT APPLICATION NUMBER: US/10/482,526A
CURRENT PILIG DATE: 2003-12-18
FRICH APPLICATION NUMBER: US 60/300,112
FRICH APPLICATION NUMBER: US 60/325,277
FRICH APPLICATION NUMBER: US 60/325,277
FRICH APPLICATION NUMBER: US 60/366,535
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US-10-972-963-70
Sequence 70, Application US/10972963
GENERAL INFORMATION:
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Best Local Similarity 70.v
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Best Local Similarity 77.8
Matches 7; Conservative
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                                      432 TRLRRSRG 439
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; ORGANISM: Oryza sativa
US-10-482-526A-576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
PCT-US04-35137-70
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LENGTH: 388
TYPE: PRT
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; ORGANISM: Pseudomonas syringae PCT-US02-091078-69335
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Best Local Similarity 66.7%;
Matches 6; Conservative
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Matches 6; Conservative
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27 RLLKNRGLK 35
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PCT-US02-09107B-74744
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034VPC
FILE REPERENCE: ELITRA.034VPC
CURRENT APPLICATION NUMBER: PCT/US02/09107B
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR APPLICATION NUMBER: 09/948,993
PRIOR FILING DATE: 2001-09-06
PRIOR FILING DATE: 2001-09-06
PRIOR PRILING DATE: 2001-02-26
PRIOR PRILING DATE: 2001-02-26
PRIOR APPLICATION NUMBER: 10/072,851
PRIOR APPLICATION NUMBER: 00/342,923
PRIOR APPLICATION NUMBER: 00/342,923
PRIOR APPLICATION NUMBER: 00/342,923
PRIOR APPLICATION NUMBER: 2001-02-608
PRIOR APPLICATION NUMBER: 2003-03-06
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PARABEL NOS: 78614
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              Score 32; DB 6; Length 441;
Pred. No. 72;
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                                                                                    2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ting, Jenny
APPLICANT: Inhoff, Michael
APPLICANT: Harton, Johnathan
APPLICANT: Harton, Johnathan
APPLICANT: Hiliams, Kristi
APPLICANT: Jich, John
APPLICANT: Jich, John
APPLICANT: O'Connor, William
APPLICANT: Moore, Christopher
APPLICANT: Moore, Christopher
APPLICANT: Davis, Beckley
APPLICANT: Conti, Brian
APPLICANT: Conti, Brian
APPLICANT: Alway, Jinghua
APPLICANT: Alw
                                                                                 1; Mismatches
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       66.7%;
70.0%;
Query Match
Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7, Conservative
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                                                                                                                                               1 TRLTRSRGLK 10
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; ORGANISM: Homo sapiens
US-10-511-989-167
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                               Query Match 64.6%; Score 31; DB 1; Length 534; Best Local Similarity 66.7%; Pred. No. 1.4e+02; Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 64.6%; Score 31; DB 1; Length 535; Best Local Similarity 66.7%; Pred. No. 1.40+02; Matches 6; Conservative 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ; ORGANISM: Clostridium acetobutylicum PCT-US02-09107B-51874
; ORGANISM: Streptococcus pyogenes PCT-US02-09107B-74744
                                                                           2 RLTRSRGLK 10
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26 RLLKNRGLK 34
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27 RLLKNRGLK 35
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-5 48 1 TRLTRSRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database

1: pirl: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

i		de (SUMMAKIES	
Result No.	Score	Query	Length	DB	ΙD	Description
-	44	91.7	596	~	S32802	apolipoprotein B -
7	44	91.7	4563	-	LPHUB	apolipoprotein B-1
٣	40	83.3	269	7	C60950	apolipoprotein B-1
4	40	83.3	779	N	JH0102	apolipoprotein B -
ς.	38	79.2	275	~	E60950	apolipoprotein B-1
9	37	77.1	309	7	AH0906	conserved hypothet
7	35	72.9	290	~	S39854	trax protein - Str
80	35	72.9	309	Н	E65112	hypothetical 34.6
6	35	72.9	309	N	E85985	hypothetical prote
10	35	72.9	309	~	B91140	
11	34	70.8	173	~	G87383	acetyltransferase,
12	34	70.8	274	N	A60950	apolipoprotein B-1
13	34	70.8	614	7	875294	ferrous iron trans
14	34	70.8	784	N	JH0101	apolipoprotein B-1
15	33	68.8	101	~	E72691	hypothetical prote
16		68.8	393	~	S48288	probable phosphopr
11	33	68.8	484	N	840051	starch synthase (E
18	33	68.8	1838	7	T18448	pathogenicity fact
19	32	66.7	208	N	E72514	hypothetical prote
20		66.7	232	Н	S28609	phosphoadenylyl-su
21		66.7		N	A98146	probable threonin
22		66.7		N	AC3142	threonine dehydrat
23	32	66.7		Н	DEHUPT	pyruvate dehydroge
24	32	66.7	412	N	E83061	hypothetical prote
25		66.7		7	B72386	hypothetical prote
56		66.7	486	N	T40901	ranbpm homolog - f
27		66.7	487	٦	LQBP34	
28	32	66.7	487	7	S06464	DNA ligase (ATP) (
53	32	66.7	206	~	AD3338	cobyric acid synth

hypothetical prote	hypothetical prote	myc-like regulator	UL56 protein - hum	hypothetical prote	hypothetical prote	leucine rich repea	pyruvate formate-1	probable DnaJ prot	CTP synthase [impo	CTP synthetase [im	CTP synthase (UTP-	CTP synthase (EC 6	3',5'-cyclic-nucle	hypothetical prote	hypothetical prote
AB1875	S76027	T14681	C48560	E83363	E84797	T17033	F69534	D96795	C95057	C86686	G97255	F97926	871626	T05448	867595
8	~	0	ч	7	0	0	~	N	7	~	~	~	~	7	7
680	1036	146	233	272	290	329	330	398	535	535	535	535	712	732	788
66.7	66.7	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6	64.6
32	32	31	31	31	31	31	31	31	31	31	31	31	31	31	31
0	-	32	33	34	35	36	37	38	39	40	41	42	43	44	5

ALIGNMENTS

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apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 332802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: 532802; MUID:92075708; PMID:1742325
A;Accession: 532802
A;Accession: S32802
A;Accession: By MUID:92075708; PMID:1742325
A;Residues: 1-596 < PAP>
A;Residues: 1-596 < PAP>
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301-C;Superfamily: apolipoprotein B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 44; DB 2;
Pred. No. 0.48;
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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1 TRLTRSRGLK 10

apolipoprotein B-100 precursor - human

N.Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C; Accession: A27860; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A264742; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R; Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sci DNA 6, 363-372, 1987

A,Title: DNA sequence of the human apolipoprotein B gene.
A,Reference number: A27850; MUID:88003974; PMID:3652907
A,Recession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Rocession: A27850
A,Residues: 1-617,'A', 619-1929,'F',1931-3318,'D',3320-3426,'T',3428-3431,'O',3433-3731,'A,Coss-references: UNIPROT:P04114; UNIPROT:P78482; UNIPROT:P78479; UNIPROT:Q9UMNO; UNI-R; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A,Title: The complete sequence and structural analysis of human apolipoprotein B-100: r. A,Recession: A25679

A;MOJecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> A;Residues: 1109-Asp was also found A;Note: 1109-Asp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

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A; Contents: disulfide bonds A; Accession: A35783
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By Deeb, S.S.; Motulaky, A.G.; Albers, J.J.

By Arcession. Asimonal Soi. U.S.A. 83, 49834986, 1985

Aymoreaula type: mRNA

Aymore
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-272,'N', 274-617,'A', 619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; Cross-treferences: GB:XV6506; NID:g3330; PIDN:CAA28191.1; PID:g34331
R; Law, S.W.; Grant, S.W.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A Molecule type: mRNA

A. Molecule type: mRNA

A. Residuaes: 1-97, 17, 99-328, 7V, 330-644, 71, 646-918, P, 920-3318, D, 3320-3426, T, 3428-94132, G, 4134-4180, E, 4182-4563 - CHE>

A. CROSS-references: GB-J02610, NID: 9178803; PIDN: AAA35549.1; PID: 9178804

A. CROSS-references: GB-J02610, NID: 9178803; PIDN: AAA35549.1; PID: 9178804

B. Morte: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides R. Proct. Natl. Acad. Sci. U.S.A. 38to, R. Y. Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; Proc. Natl. Acad. Sci. U.S.A. 33, 5678-5682, 1986

A. Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein A. Accession: A24320, MUID: 86287319; PMID: 3461454
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A; Residues: 1-97, 'I', 99-617, 'A', 619-941, 'YYIWSLPPKP', 951-1138, 'PTGRLPNCFSNGLICYSLWIHSFQE
A; Cross-references: GB M44081, NTD:918795; PIDN AAA51752.1; PID:9553189
R; Law, S.W., Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S. A. 82, 8340-8344, 1985
A; Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A; Reference number: A24684; MUID:86094221; PMID:3001697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 485-617, 4',619-1044 <LA2>
A; Croster. 48-617, 4',619-1044 <LA2>
A; Croster. A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki
Proct. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a CDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; MUID:86149325; PMID:3513177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S',1272-1866,'G',1868-2036,'N', 2
4189-4220,'M',4222-455 a.LAM>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
B; Biol. Chem. 251, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
            human apolipoprotein B-100.
Title: Complete cDNA and derived protein sequence of P
Reference number: A93639; MUID:87016385; PMID:3763409
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Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Atherosclerosis 58, 277-289, 1985
A.Title: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A.Reference number: A90084; MUID:86130855; PMID:3841481
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residence: 3846-4298 A.SHO>
B.Pfizzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A.Title: Isolation, expression and characterization of a human apolipoprotein B 100-speci
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: 4339, 4339, 4563 < PFI>
A;Cross-references: GB:M36676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
A;Reference number: A24738; MUID:86042646; PMID:2932736
A;Accession: A24738
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A; Accession: A40133
A; Accession: A40133
A; Accession: B4013
A; Cross-references: GB: MIB036; MID: G178799; PIDN: AA51754.1; PID: G178800
A; Accession: B40133
A; Accession: A40133
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A; Residues: 2169-2179 < HOS>
A; Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species hown represents the carboxyl end of apolipoprotein B-48
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250K apoB-48, CAA encoding 2180-Gln is substituted by the stop codon TAA, R; Asnag, C.; Kim, T.W.; Wengy, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human again Reference number: A35783; MUID:90319144; PMID:2115173
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A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
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A; Residues: 2129-2179, 2181-2235 <HA2>
A; Residues: 2129-2179, 2181-2235 <HA2>
A; Croser references: GB.M18471
A; Experimental source: intestine
A; Note: this mRNA from intestine includes a stop codon created by RNA editing in place
A; Note: Acids Res. 13, 6937-6953, 1986
Nucleic Acids Res. 13, 6937-6953, 1986
A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of A; Reference number: A24269; MUID:86041888; PMID:3903660
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A; Residues: 3056-3159 <MEH>
A; Cross-references: GBX30345; NID: g28783; PIDN: CAA26850.1; PID: g929609
A; Cross-references: GBX30345; N.; Law, S.W.; Meglin, N.; Brewer Jr., H.)
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reference number: A29659; MUID:88049670; PMID:2445342
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A; Molecule type: DNA
A; Residues: 1-779 <SMI.>
A; Residues: 1-779 <SMI.>
A; Cross-references: UNIPROT: 060536; GB: M35187
A; Note: this is a revision to the sequence from reference JH0101
R; Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of an A; Reference number: JH0101; MUID: 90236327; PMID: 2332175
A; Contents: annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C:Keywords: atherosclerosts; calcium; cholesterol metabolism; chylomicron; glycoprotein F;415-445/Region: receptor binding F;646-656/Region: receptor binding
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C;Species Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B60950
R;Law, A.; Scott, J.
J;Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD: A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: E60950
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A;Residues: 1-275 < LAM>
A;Cessareserences: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0906
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar b. S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica
                                                             C;Species: Mesocricetus auratus (golden hamster)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
R;Smith, T.J.
submitted to GenBank, June 1990
A;Reference number: A38864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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Pred. No. 4.1;
1; Mismatches
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Pred. No. 3.9;
0; Mismatches
                                            (fragment)
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A,Gene: apoB
C,Superfamily: apolipoprotein B
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Best Local Similarity 80.0°
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Best Local Similarity 80.0
Matches 8; Conservative
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642 SRLTRKRGLK 651
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                                                                                                                                                A,Rocession: A22006
A,Rocession: B22006
A,Rocession: A,Rocession: B,R. ; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C.; A,Ritle: Structure of the human apolloporotein B gene.
A,Rocession: R, Fitzner, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 368, 419-425, 1987
A,Fitle: Studies on the organization of the human apolloporotein B 100 gene.
A,Rocession: B-100 heparin-binding sites.
A,Fitle: Man apolloporotein B-100 heparin-binding sites.
A,Fitle: Molipoprotein B-100 heparin-binding protein.
A,Rocession: B, D,M.; Mok, T.
Biochem. Blophys. Res. acalcium binding protein.
A,Rocession: B, D,M.; Mok, T.
Biochem. Blophys. Res. 13, 491-499, 1986
A,Fitle: Apolloporotein B is a calcium binding protein.
A,Rocession: B, D,M.; Mok, T.
Biochem. Blophys. Res. 13, 8913-892, 1987
A,Fitle: Molipoprotein B is a calcium binding protein.
A,Rocession: B, D,M.; Mok, T.
Biochem. Blophys. Res. 13, 8913-892, 1986
A,Fitle: Molipoprotein B is and Calcium binding Protein.
A,Rocession: B, Bylles B, Bylles B, Bylles B, A,Fitle: Molecular cloning of human apolipoprotein B cDNA.
A,Rocession: 137180
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C;Species: Mesocricetus auratus (golden hamster)
C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Cocssion: C60950
R;Law, A.; Scott, J.
J;Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Recession: C60950
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-269 < LAM>A;Cocssion: C60950
A;Residues: 1-269 < LAM>A;Cocssion: C60950
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
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                                                                                                A;Title: Human apolipoprotein B: partial amino acid sequence A;Reference number: A22006; MUID:84208786; PMID:6373369
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80.0%; Pred. No. 1.5;
cive 1; Mismatches 1
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216 SRLTRKRGLK 225
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Best Local Similarity
Matches 9; Conserv
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170 TQLARQRGLK 179
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Best Local Similarity
7; Conserv?
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          :Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: AH0906
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A/Molecule type: DNA
A/Residues: 1-290 <BRO>
A/Residues: 1-290 <BRO>
Corest-references: UNIPROT:Q06258; EMBL:X72857; NID:g288432; PIDN:CAA51379.1; PID:g5816
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enter A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Recession: AH0906
A;Retaus: preliminary
A;Molecule type: DNA
A;Residues: 1-309 <PAR>
A;Residues: 1-309 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07846.1; PID:g16504394; GSPDB:GN00176
C;Genetics:
A;Gene: STY3508
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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C;Species: Streptomyces coelicolor
C;Accession: S39654; S32232
R;Brolle, D.F.; Pape, H.; Hopwood, D.A.; Kieser, T.
Mol. Microbiol. 10, 157-170, 1993
A;Title: Analysis of the transfer region of the Streptomyces plasmid SCP2*.
A;Reference number: S39853; MUID:95058174; PMID:7968512
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Pred. No. 17;
1; Mismatches 0; Indels
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Pred. No. 7;
1; Mismatches 2
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70.08;
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87.5%;
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Best Local Similarity 70.0
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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Matches 7; Conserv
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Decides: Escherical protein yhoc [imported] - Escherichia coli (strain O157:H7, substrain EDL93. C.Species: Escherichia coli (C.Species: Escherichia coli (C.Spec
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Cispecies: Escherichia coli
Cibate: 18-Vul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Ciscossion: B91140
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Byasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
BNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
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A;Residues: 1-309 <HAY>
A;Cross-references: UNIPROT:P45476; GB:BA000007; PIDN:BAB37513.1; PID:g13363563; GSPDB:C
A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acetyltransferase, GNAT family [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: 687383
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B;Nierman, W.C.; Feldblyum, T.V.; Daulsen, I.T.; Nelson, K.E.; Gisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
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C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: EC84090
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
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Best Local Similarity 70.0
Matches 7; Conservative
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C;Species: Mus musculus (house mouse)
C;Species: Musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0101; S33128; D60950
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of againetence number: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A,Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AjGene: MGI:Apob
AjCross-references: MGI:88052
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein,
F;435-445/Region: receptor binding
F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein APE0949 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72691
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takai awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; EDNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy.
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Molecule type: DNA,
KResidues: 1-101 «KAN»
A;Cross-references: UNIPROT:Q9YDG4; DDBJ:AP000060; NID:g5104188; PIDN:BAA79933.1; PID:g
A;Experimental source: strain K1
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                                              Length 614;
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                                                  DB 1;
56;
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Pred. No. 71;
1; Mismatches
                                                                                                                           3; Mismatches
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                                                  Score 34;
Pred. No. E
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A.Molecule type: DNA
A.Residues: 1-784 <SMI>
Cross-references: UNDROT:Q61314; GB:M35186
R.Smith, T.; Hautamaa, D.; Maeda, N.
submitted to the EMBL Data Library, May 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein B-100 - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 427-531,'S',533-700 <LAW>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Reference number: 833128
A, Accession: 833128
A, Accession: 833128
A, Molecule type: DNA
A, Residues: 1-531,'S', 533-784 <SM2>
A, Cross-references: EMBL:X15191
R, Law, A, Scott, J.
J, Lipid Res. 31, 1109-1120, 1990
                                                  70.8%;
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Best Local Similarity 70.v.
                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                361 TRVMRSRGMR 370
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647 SRLMRKRGLK 656
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                                                                                 Best_Local Similarity
Matches 6; Conserv
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A;Status: preliminary
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                                                      Query Match
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E72691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein B-100 - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: Janec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A60950
R;Law, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL
A;Reference number: A60950; MUD:90324804; PMID:2373961
A;Accession: A60950
A;Accession: A60950
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A;Accession: Accession: Ac
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A; Accession: S75294
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT:P73182; EMBL:D90904; GB:AB001339; NID:g1652225; PIDN:BAA1726
A; Molecitics:
A; Molecitics: A; Molecule sequence was submitted to the EMBL Data Library, June 1996
C; Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolo
C; Superfamily: ferrous iron transport protein B; translation elongation factor Tu homolo
F; 19-114/Domain: translation elongation factor Tu homology < F19-114/Domain: translation elongation factor Tu homology < F19-122/Region: nucleotide-binding motif A (P-loop)
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C;Accession: S72294
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87349; MUID:21173698; PMID:11259647
A;Accession: G87349
A;Accession: G87349
A;Residues: 1-173 <STO>
A;Residues: 1-173 <STO>
A;Gross-references: UNIPROT:Q9A9B1; GB:AE005673; NID:g13422385; PIDN:AAK23067.1; GSPDB:(C;Genetics: A;Gene: CC1083)
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N;Alternate names: protein slr1392
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S75294
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Pred. No. 17;
1; Mismatches 1; Indels
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77.8%;
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Best Local Similarity 77.8
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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C;Genetics:
A;Gene: APE0949
C;Superfamily: Aeropyrum pernix hypothetical protein APE0949
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0; Gaps Query Match 68.8%; Score 33; DB 2; Length 101; Best Local Similarity 100.0%; Pred. No. 16; Matches 7; Conservative 0; Mismatches 0; Indels

0,

3 LTRSRGL 9 ||||||| 74 LTRSRGL 80 ò

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Search completed: December 29, 2004, 12:39:03 Job time : 10.6591 secs

Scoring table:

Searched:

Database

Perfect score:

Sequence:

OM protein

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Run

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Q8fd65 escherichia
Q06528 streptomyce
Q8vwd2 streptomyce
Q8vwd2 streptomyce
Q8vwd2 streptomyce
Q83jf2 shigella f1
Q88c72 pseudomonas
Q9384 candida boi
G6nac6 rhodopseudo
Cae26702 rhodopseu
                              O52565 amycolatops
Q8fd65 escherichia
                  Aas07756 amycolato
 Q7bud9 amycolatops
                                                                                                                                                                                                                                                                                                                                                                                                                                         Actus vociferans (Spix's owl monkey).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Platyrrhini; Cebidae; Actinae; Actus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apolipoprotein B (Fragment).
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUB=Liver;
MEDLINE=92075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchlor G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 414;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                             414 AA
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                              052565
Q8FD65
Q06258
Q8VWD2
YHCC_ECOLI
Q07UBF4
Q83JF2
Q88C72
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QENACE
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                                                                                                                                                                                                                                                                                                                                                                             Created)
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Q7BUD9
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Created)
01-N0V-1986 (Rel. 03, Last sequence update)
05-NUL-2004 (Rel. 44, Last annotation update)
Apolipoprotein B-100 precursor (Apo B-100) (Contains: Apolipoprotein B-48) (Apo B-48)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
metabolism in the cynomolgus monkey: evidence for post-
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PIR; A27850; LPHUB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
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                            transcriptional regulation.",
Biochim. Biophys. Acta 1086:326-334(1991)
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EMBL; X15737; CAA33755.1;
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SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M., Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
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MEDLITE=85300528; PubMed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B. structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
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SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=86641888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz B., Lusis A.J.,
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
SEQUENCE FROM N.A. MEDINE-1763409; MEDLINE-17016385; Pubmed=1763409; Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J., Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.; "Complete cDNA and derived protein sequence of human apolipoprotein
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MEDLINE-86093680; PubMed=3841204;
Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O.,
Bjursell G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=87041416; PubMed=3464946;
MEDLINE=87041416; PubMed=3464946;
Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J.,
Lie N., Brewer H.B. Jr.;
"Human liver apolipoprotein B-100 cDNA: complete nucleic acid and
derived amino acid sequence.";
Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-88003974; PubMed=3652907;
Ludwig E.H., Blackhart B.D., Flerotti V.R., Caiati L., Fortier C Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
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MEDLINE-87161758; Pubmed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.
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Nucleic Acids Res. 13:8813-8826(1985).
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MEDLINE=85270450; PubMed=3860836;
Deeb S.S., Motullary A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
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                                                                                                                                                                                                                        PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDLINE=80018019; PubMed=3659919;
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Silberman S.R., Cai S.-J., Deelypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.,
"Apolipoprotein B-48 is the product of a messenger RNA with an organ-
specific in-frame stop codon.";
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                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87019351; PubMed=3773997;
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Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
"Levy-Wilson B., Scott J.;
"Complete protein sequence and identification of structural domains human apolipoprotein B.";
                                                                                                         SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
MEDLINE=86287319; PubMed=3461454;
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"Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien P., Roizes G.; "Decection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene."; Hum. Genet. 86:91-93(1990).
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McCarthy B.J.;
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                                                                 apolipoprotein B.";
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[12]
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SEQUENCE OF 1-291 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PALMITOYLATION OF CYS-1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 323:734-738(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALCIUM-BINDING DATA.
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MEDLINE-97403938; PubMed-9259199;
Rabes J.P., Varret M., Saint-Jore B., Brlich D., Jondeau G.,
Krempf M., Giraudet P., Junien C., Boileau C.;
Framilial ligand-defective apolipoprotein B-100: simultaneous
detection of the ARG3500-->GLN and ARG3531-->CYS mutations in a Prench
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hum. Genet. 102:44-49(1998).

-!- FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.

-!- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                          MEDIINE=95190020; PubMed=7883971; Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.; Frantilal ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
                                                                                                                                                                                                                                                                                                                                                            VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
                                                                                                                                                                                                                                                                                                                                                                                                                                         Poirier O., Ricard S., Behague I., Souriau C., Evans A.E., Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F., Detection of new variants in the apolipoprotein B (Apo B) gene by
                                                           gene at position 8344.";
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Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
hypocholesterolemia.";
Hum. Genet. 102:44-49(1998).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Last annotation update)
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0; Mismatches
MEDLINE=91016974; PubMed=2216805;
Huang L.-S., Gavish D., Breslow J.L.;
"Sequence polymorphism in the human apoB
Nucleic Acids Res. 18:5922-5922(1990).
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97044521; PubMed=8889592;
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SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer Compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AFS48435; AAP97391.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nyctimene albiventer (Common tube-nosed fruit bat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-22761261; PubMed=12878460;
MEDLINE-27561261, Koepfil K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Chiroptera, Megachiroptera, Pteropodines, Pteropus.

Pteropodinae, Pteropus.
                                                                                                                                               2; Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.3%; Score 40; DB 2; Length 436;
80.0%; Pred. No. 11;
ive 1; Mismatches 1; Indels
                                                                                      432
48171 MW; F27B7AB39604732C CRC64;
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436 436
436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                                                                                                                       436 AA
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                                                                                                                                               Score 40; DB
Pred. No. 11;
                                                                                                                                                                                  1; Mismatches
             Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AY243375; AAP50763.1; -.
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                           83.3%;
                                                                                                                                                            Local Similarity 80.0
les 8; Conservative
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NCBI TaxID=48988;
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279 SRLTRKRGLK 288
                                                                                                                                                                                                                     1 TRLTRSRGLK 10
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                                                                                                       432 AA;
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                                                  Lipoprotein.
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SEQUENCE 436
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Q7YQMB;
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Matches
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TremBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Bullipoprotein B (Fragment).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalla; Butheria, Rodentia, Sciurognathi; Sciuridae, Petauristinae,
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22761261; PubMed=12878460; Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
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MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; Robpfil K.-P., Wayne R.K., Springer M.S.;
Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
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0
                                                                                                                                                                                                                 Length 4563;
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80.0%; Pred. No. 11;
iive 1; Mismatches 1; Indels
                                                                                                                                                                      4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421
46747 MW; D47B77BD4F864FD1 CRC64;
EMBL; AY324608; AAP72970.1; -. GO; GO:00519; F:1ipid transporter activity; IEA. GO; GO:000569; P:1ipid transport; IEA. InterPro; IPR009454; DUF1081.
InterPro; IPR00144; Lipid_transport_N. PEan; PF06448; DUF1081.
PEan; PF06448; DUF1081; 1. PEAN; PF06448; Vitellogenin_N; 1. SMART; SM0638; LPD_N; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                             Score 44; DB 2;
Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                         421 AA.
                                                                                                                                                                                                                                                 0; Mismatches
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                                                                                                                                                                                                         91.7%;
90.0%;
                                                                                                                                                                                                                                                 9; Conservative
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Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                     3385 TRLTRKKGLK 3394
                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                    1 TRLTRSRGLK 10
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Matches 9: Conserv
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NON TER
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SEQUENCE 42
                                                                                                                                                      Lipoprotein.
SEQUENCE 4:
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Q7TN68;
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SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.';
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AFS48417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AY291369; AAPS0757-1, ...
InterPro: IPR000871; Beta lactamase A.
PROSITE; PS00146; BETA_LACTAWASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                          Agouti paca (Paca).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Agoutidae, Agouti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apolipoprotein B (Fragment).
Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.3%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 11; indels ive 1; Mismatches 1; Indels
                                Length 445;
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445 445
445 AA, 49721 MW; 34AF7ABB90F121EF CRC64;
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
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                                                                                                                                                                                                                                                      01-00T-2003 (TrEMBLrel. 25, Created)
01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01.WAR-2004 (TrEMBLrel. 26, Last annotation update)
                              Match 83.3%; Score 40; DB 2; Local Similarity 80.0%; Pred. No. 11; les 8; Conservative 1; Mismatches
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MEDLINE-2761261, bubMed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243383; AAP50771.1;
                                                                                                                                                                                                                                                                                                                      01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Rousettus amplexicaudatus (Common rousette).
Rousettus amplexicaudatus (Common rousette).
Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Pteropodinae; Rousettus.
NCBI_TAXID=58083;
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Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chaetophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Chaetophractus.
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                                                                                                Score 40; DB 2; Length 438;
Pred. No. 11;
1; Mismatches 1; Indels
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Pred. No. 11;
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438
48734 MW; 2BD85BCBF4E2CC41 CRC64;
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438 438
438 AA, 48597 MW, 41C890DEAF95C872 CRC64;
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EMBL; AF548436; AAP97392.1;
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281 SRLTRKRGLK 290
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281 SRLTRKRGLK 290
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MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

Maeda N.;

"Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";

Gene 87:309-310(1990).

PERL; M35187; AAA37059.1; -.

PIR, C60950, C60950.
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
And phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243368; AAP50756.1; -.
                                                                                                                                                                                            01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolioporotein B (Fragment).
Brethizon dorsatum (North American porcupine).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Erethizontidae;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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   Score 40; DB 2; Length 445;
Pred. No. 11;
1; Mismatches 1; Indels
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49617 MW; 9572FE5F5E7625F2 CRC64;
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86625 MW; E371D1B2079D8F7E CRC64;
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SEQUENCE 441
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80.0%; Pred. No. 21;
tive 1; Mismatches 1; Indels
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Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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1 TRLTRSRGLK 10

642 SRLTRKRGLK 651

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December 29, 2004, 12:10:41; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:*geneseqp2004s:* A_Geneseq_23Sep04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

on:	Apo-B100	Apo-B100	Apo B bin	Apo B 100	Apolipopr	ApoB-100	Heparin b	Apo B 100	Apo B 100	Human apo	Nucleic a	Human apo	Nucleic a	Peptide #	Human liv	Human apo	Sequence	Human apo	Human Apo	Apolipopr	Amino aci	Human apo	Human Pro	Human apo	Human ali
Description	Aay30687	Aay30682	Aaw57205	Aaw57207	Aaw41261	Aaw96892	Abj37575		Aaw57209	Aae14541	Aaw96876	Aaw64587	Aaw96845	Abb37687	Abg52504	Aar72704	Aar34031	Adj 57400	Aay31237	Aaw41262	Aaw96826	Aau98981	Add48677	Aao15893	Abr40253
QI	AAY30687	AAY30682	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981	ADD48677	AA015893	ABR40253
DB	7	~	7	N	N	7	ø	7	7	ഗ	7	7	~	4	4	0	~	œ	~	7	~	S	7	Ŋ	9
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% Query Match	100.0	93.9	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8	91.8
Score	49	46	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45	45
Result No.	7	7	m	4	2	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

	Aaw41260 Apolipopr
ABU79140 ADF43408 ADF43408 ADF118871 ADF118870 ADF33447 ADF33447 AAY30686 AAY30686 AAY30686 AAY30686 AAY30686 AAY30688 AAY30688 AAY30692 AAY310688 AAW57206	AAW41260
0 C B B B B B B B B B B B B B B B B B B	N
4 4 5 6 5 3 4 4 4 5 6 5 3 3 4 4 5 6 5 3 3 4 4 5 6 5 3 3 4 5 6 5 5 5 6 5 5 6 5 6 5 6 5 6 5 6 5 6	77
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0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	40
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ALIGNMENTS

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Ä. AAY30687 standard; peptide; 10 99WO-US004805. 98US-0077618P. Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Synthetic. Homo sapiens. WO9946598-A1. 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999. AAY30687; AAY30687

LID AAY30687

AAY30687 RESULT 1

Claim 17; Page 57; 70pp; English.

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate artheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgent non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo sassay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can

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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds which affect binding of low density lipoprotein with proceedlycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                        Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                               Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                   100.0%; Score 49; DB 2; Length 10; larity 100.0%; Pred. No. 0.019; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                            AAY30682 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US004805
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                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA.
                                                                                                                                               1 TRLTRORGLK 10
                                                                                                                                                                      1 TRLTRORGLK 10
                                                                                        Query Match
Best Local Similarity
10, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-551509/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             atherosclerosis.
                                                                              Sequence 10 AA;
                                                                                                                                                                                                                                                                           17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                     AAY30682;
                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which and material activated from amino acids 3388 to 3367 of apos100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (EG). The method can be used for identifying compounds which farupt LDL-EG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-luman animals and mammals which express human apo-B100 can be used as an in vivo model system for the structural relations and in vivo model system for the cherosclerosis and/or LDL-EG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether fow or a drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in mammal
Claim 17; Page 57; 70pp; English.
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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle of the present that at least 1 binding site for an apo B protein receptor and at least 1 lipophils competent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media sepecially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B contained and tends to aggregate, to provide binding sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                               Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide binding to apo B protein delivering drugs to cancer cells
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     Length 10;
                                 0; Indels
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Pred. No. 0.12;
1; Mismatches 0; Indels
 Score 46; DB 2;
Pred. No. 0.069;
                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
                                                                                                                                                                     AAW57205 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                 Apo B binding site peptide 2.
93.9%;
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90.0%;
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                              9; Conservative
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TRLTRERGLK
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                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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Query Match
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Best Local S
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Matches
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AAW57207;

AAW57207

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This sequence is an example of the peptide of the invention. It has the formula (1), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). 21-KAQ-XI-KYAKHRHS-X2-T-22 (1) X1 = S or Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (as); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 as a Compositions containing the peptide, are simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated processes, specifically to prevent or reduce blood coagulation (e.g. thibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits active the prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                                                      Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   smaller than apoB-100, they act more quickly
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                                                                                Apolipoprotein B-100 fragment.
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                          19-MAY-1998
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                                                                                                                                                                                                                                                                                  Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-actually occurring, receptor.competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 ceptide component that has at least 1 binding sequence with at least 1 inpophilic substituent. Also described in the receptor and at least 1 lipophilic substituent. Also described in the receptor and at least 1 lipophilic substituent. Also described in the receptor and at least 1 lipophilic substituent. Also described in the competences: KABYKKWKHRH (1) or TTRLTRKRGIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B proctein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete specially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete after the complete specially as the structure media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete after the complete special s
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                                                                                                                                                                                                                                                                                                       Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
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                                                                                                                                                                                                                                                    Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "attached to retinoic acid"
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Pred. No. 0.14;
1; Mismatches
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                                                                             AAW57207 standard; peptide; 13 AA.
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90.0%;
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Halbert

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Gaps

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Length 15; 0; Indels Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;

AAW41261;

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AAW41261

Matches

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Baillie
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           20-JUL-2001; 2001US-0306726P
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Best Local Similarity
9, Conserv?
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7 TRLTRKRGLK
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                                                                                                                                                                                                                                                                                                                                                            Sequence 20 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                 invention
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                                                                                                                                                                                                                                                                                                                                                                                                          AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a The present sequence can be used in the composition of the invention. The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic calls. The composition is used to deliver nucleic acids to eukaryotic calls, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                                      Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                              Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                                Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                              (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                   97US-00874807,
98US-00079030,
                                                                                                                                                        98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUL-2002; 2002WO-US023419.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                           WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2003007689-A2
                                                               Homo sapiens
                                                                                                                                                     10-JUN-1998;
                                                                                                                                                                                  13-JUN-1997;
14-MAY-1998;
                                                                                         WO9856938-A1
                                                                                                                        17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                              Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2003
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Best Loc Matches

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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                    Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDb; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB 6; Length 20;
Pred. No. 0.2;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "attached to cholesterol"
Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW57208 standard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                 Disclosure, Fig 2; 79pp; English.
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KABYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete also B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide binding to apo B protein delivering drugs to cancer cells
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                     91.8%; Score 45; DB 2; Length 22; 90.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising
receptor - useful as, e.g. vector for
                                                                                                                                                                                                                                                                        affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owens MD, Baillie G;
                Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW57209 standard; peptide; 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-GB002610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRORGLK 10
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 9; Conserv
                                                                                                                                                                                                                                                                                                       Sequence 22 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAWS7209;
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Matches
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

Claim 13; Fig 7; 73pp; English.

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particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KADYKKWGHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-targeting veceptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDE), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDE. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDE. In a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                      2; Length 22;
                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                    Score 45; DB 2;
Pred. No. 0.22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAE14541 standard; peptide; 34 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                  91.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ARKT-) ARK THERAPEUTICS LID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                       Local Similarity 90.0
                                                                                                                                                                                                                                                                                                                                                                                     TRLTRORGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                        TRLTRKRGLK 16
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                                                                                                                                                                                                                                                               Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lipoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide p62
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                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                       Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoprotein sequence can be used in the composition of the invention. The present specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of fibrosis and arteriosclerosis
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                         Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                Length 34;
                                                                                                            0; Indels
                                                                           Score 45; DB 5;
Pred. No. 0.33;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore JP;
                                                                                                                                                                                                                                     AAW96876 standard; peptide; 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                      Query Match
Best Local Similarity 90.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US011927.
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                                                                                                                                                                                                                                                                                               (first entry)
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Best Local Similarity 90.07
                                                                                                                                     1 TRLTRORGLK 10
                                                                                                                                                      25 TRLTRKRGLK 34
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                                           Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1998;
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14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment.
                                                                                                                                                                                                                                                                 AAW96876;
                                                                                                                                                                                                        RESULT 11
AAW96876
8233
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Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.

Example 2; Page 9; 18pp; German.

Schenk V;

Lang H,

Moritz B, Kiessig S,

(IMMO) IMMUNO AG.

WPI; 1998-416142/36.

98EP-00890007. 97AT-00000044

12-JAN-1998; 13-JAN-1997;

Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.

Homo sapiens

EP857973-A2. 12-AUG-1998.

Human apolipoprotein peptide fragment #1.

(first entry)

23-OCT-1998

AAW64587;

AAW64587 standard; peptide; 37 AA

TRLTRKRGLK 20

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Consequence of a mutated protein in a sample that may also detect the presence of a mutated protein in a sample that may also contain the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are vein thrombosis), mutations in apolipoprotein (apo) genes (certain alleles of apoB indicates increased risk of deep alleles of apoB indicates increased risk of developing Alzheiner's alleles of aboB indicates increased risk of cardiovascilar disease), thermostable 5.10-methyleneterrahydrofolate reductase mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase particularly suited to routine screening. It also allows mutant protein in a sample to be quantified
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Pred. No. 0.35;
1; Mismatches
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90.0%;
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Best Local Similarity 90.0
Matches 9; Conservative
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91.8%; Score 45; DB 4; Length 343; 90.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID No 31152.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W,
                                                                                                                                                                                                                                                                                                        ; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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2000US-0204456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-023458P.
                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532366.
21-SEP-2000; 2000US-023687P.
27-SEP-2000; 2000US-02363599.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                           30-JAN-2001; 2001WO-US000669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 343 AA;
WO200157277-A2
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03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
04-OCT-2000; 2
                                                                                                                                                                                                                                                                                                                   04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100) a major apoprotein component of very-low density lipoproteins (VDL), intermediate density lipoproteins (VDL), intermediate density lipoprotein (IDL), low density lipoproteins (LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The present appolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapoutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                                                                                                                                                                                                                                          Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apollpoprotein; Dinding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                 Nucleic acid binding domain from apoB-100
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TRLTRKRGLK 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1998;
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14-MAY-1998;
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Best Loc Matches

RESULT 14 ABB37687

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(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 11109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences

Sequence 343 AA;

Gapa ö Query Match 91.8%; Score 45; DB 4; Length 343; Best Local Similarity 90.0%; Pred. No. 2.7; Matches 9; Conservative 1; Mismatches 0; Indels

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1 TRLTRORGLK 10 ò g

169 TRLTRKRGLK 178

Search completed: December 29, 2004, 12:28:49 Job time : 62.0227 secs

us-09-823-418-6.rag

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

December 29, 2004, 12:15:57 ; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec

US-09-823-418-6 1 TRLTRORGLK 10 Perfect score: Sequence: Title:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 79:* Database

1: pirl: * 2: pirl: * 3: pirl: * 4: pirl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	cripti	apolipoprotein B -	ipoprotein	apolipoprotein B-1		hypothetical 34.6	hypothetical prote		apolipoprotein B-1	conserved hypothet	starch synthase (E	hypothetical prote	apolipoprotein B-1	probable phosphopr	_		dihydroorotase (dh	cobyric acid synth	ical	soluble starch syn	starch synthase DU	pyruvate formate-1	hypothetical prote	adenylate transloc	starch synthase (E	glycogen synthase	starch synthase (E	replicative DNA he	cative DNA	replicative DNA he
	DI	S32802	LPHUB	C60950	JH0102	E65112	E85985	B91140	E60950	AH0906	S40051	E83061	A60950	S48288	JH0101	AC2737	A97518	AB2103	H86250	T07663	T01266	F69534	B75286	T05350	C64119	B95130	H98000	D97492	AC2710	AG3437
	DB	7	н	~	~	Н	~	0	~	~	7	~	N	7	~	7	7	N	7	7	~	Н	7	~	~	~	7	7	7	7
	ng	965	4563	269	779	309	309	309	275	309	484	412	274	393	784	430	430	493	1025	1230	310	330	332	392	476	477	477	498	498	501
*	당	91.8			•	81.6	•	81.6	79.6	9.6	77.6	75.5	71.4	71.4	71.4	69.4	69.4	69.4	69.4	69.4	67.3	67.3	67.3	67.3	67.3	۲.	7	67.3	7	7.
	Score	45	45			40	40	40	39	39	38	37	35	35	35	34		34	34	34	33	33	33	33	33	33	33	33	33	33
1	No.	-	7	3	4	2	9	7	80	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical prote	starch synthase DU	acetyl-CoA carboxy	acetyl-CoA carboxy	ribosomal protein	salivary glue prot	salivary glue prot	acetyltransferase,	exopolyphosphatase	molybdenum cofacto	probable glycosylt	starch synthase (E	mannonate oxidored	D-mannonate oxidor	fructuronate reduc	cytochrome c-type
AB1875	T01265	T42531	T38906	S78289	S12607	S33822	G87383	AE2652	T46858	B95936	AI0995	E86130	B91289	S56548	E57987
N	7	7	7	~	~	7	~	7	~	~	~	0	7	7	-
680	1674	2279	2280	83	107	112	173	341	394	427	477	486	486	486	552
67.3	67.3	67.3	67.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3
		_	_	~	~	2	32	32	32	2	2	~	~	r	2
33	33	m	33	m	m	n	٣	e	(")	۲۰,	e	m	m	m	m

ALIGNMENTS

apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession. 832802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Biophys. Acta 1086, 326-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r A;Reference number: 832802; MUID:92075708; PMID:1742325
A;Accession: 832802
A;Status: A;Molecule_type: mRNA A;Residues: 1-556 cPAP> A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301-C;Superfamily: apolipoprotein B ö Gaps ô Length 596; 0; Indels Score 45; DB 2; Pred. No. 0.43; 1; Mismatches 91.8%; 90.0%; 9; Conservative Query Match Best Local Similarity Matches

226 TRLTRKRGLK 235 1 TRLTRORGLK 10 원 ò

apolipoprotein B-100 precursor - human

N.Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Homo sapiens (man)
C;Species: Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25679; A25263; A25267; A25266; A24320; A24684; A23817; A25774; A2.
A4452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Scr

A,Title: DNA sequence of the human apolipoprotein B gene.
A,Reference number: A27850; MUID:88003974; PMID:3652907
A,Accession: A27850; MUID:88003974; PMID:3652907
A,Accession: A27850
A,Accession: A27870
A,A

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-App was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

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Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E., Atherosclerosis 58, 277-289, 1985
Aritile: Molecular cloning of human LDL apolipoprotein B CDNA. Evidence for more than on A; Reference number: A90084; MUID:86130855; PMID:3841481
A; Residues: 3846-4298 «SHO»
A; Molecule type: mRNA
A; Residues: 3846-4298 «SHO»
B; Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A; Fitzner isolation, expression and characterization of a human apolipoprotein B 100-spect A; Reference number: A25572; MUID:87076044; PMID:3024665
A; Accession: A25572
A; Molecule type: mRNA
A; Residues: 4219-4337, 8', 4339-4563 «PFI»
A; Cross-references: GB:M36676
A; Cross-references: GB:M36676
B; Cr.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T..., Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A; Accession: A4738; MUID:86042646; PMID:2932736
A; Accession: A4738; MUID:86042646; PMID:2932736
A; Accession: A4738; MUID:86042646; PMID:2932736
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Ajaccession: A24;138
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Ajaccession: A24;138
Ajaccession: A24;138
Ajaccession: A24;138
Ajaccession: B40;139:11,'1',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39]
AjTille: Apolipoprotesin B-48 is the product of a messenger RNA with an organ-specific in Ajaccession: B40133
Ajaccession: A240133
Ajaccess
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A,Residues: 28-41,76-97,'I',99-100,175-193,206-215,239-249,259-266,357-399,455-490,512-5
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A; Residues: 1219-2179; 2181-2235 < HA2>
A; Residues: 1219-2179; 2181-2235 < HA2>
A; Resterences: GB: MB471
A; Experimental source: intestine
A; Note: this mRNA from intestine includes a stop codon created by RNA editing in place
B; Mehrabian, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.P.; Kirchgessner,
Nucleic Acids Res. 13, 6937-6953, 1985
A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of
A; Reference number: A24269; MUID: 86041888; PMID: 3903660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stop codon in human intestine
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A; Residues: 3056-3159 eMEH>
A; Cross-references: GB:X33045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A; Cross-references: GB:X33045; NID:g28783; PIDN:CAA26850.1; PID:g929609
R; Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.:
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A; Title: Identification of a novel in-frame translational stop codon in A; Reference number: A29659; MUD:88049670; PMID:2445342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A28002
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A,Reference number: A25774; MUID:85270450; PMID:3860836
A,Reference number: A25774; MUID:85270450; PMID:3860836
A,Reseasion: A25774
A,Wolecule type: mRNA
A,Residues: 709-791, SSSWKAASHGCPHSAGD', 810-906 cDEE>
A,Cross-references: GB:K03175; NID:9178821; PIDN:AAA51759.1; PID:9178822
R,Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
Gene 49, 29-51, 1986
A,Title: Analysis of the human apolipoprotein B gene; complete structure of the B-74 reg
A,Reference number: A91565; MUID:87191999; PMID:2883086
A,Reference number: A91565; MUID:87191999; PMID:2883086
A,Reference number: A91565; MUID:87191999; PMID:3883086
A,Residues: 1282-2721, 2742-3290, 'L',3292-3336, 'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A,Rocsesion: A26721
A,Rocsesion: A2671; MUID:88050832; PMID:3676265
A,Title: Structural comparison of human apolipoproteins B-48 and B-100.
A,Reference number: A29671; MUID:88050832; PMID:3676265
A,Rocsesion: A29671; MUID:88050832; PMID:376265
A,Rocsesion: A28671; MUID:87731; PIDN:AAA51741.1; PID:9178732
A,Cross-references: GB:M17367; NID:9178731; PIDN:AAA51741.1; PID:9178732
                                                                                                                                                                                                                                                                        A Molecule type: mRNA
A;Residues: 1-272, 'N', 274-617,'A', 619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A;Residues: 1-272, 'N', 274-617,'A', 619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A;Cross-references: GB.X04506; NII:934330; PIDN:CAA28191.1; PID:934331
R;Law, S.W.; Grant, S.M.; Higuchi, K.; Hospattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A;Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A;Reference number: A94134; MUID:87041416; PMID:3464946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule trype: mRNA
A; Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S', 1272-1866,'G', 1868-2036,'N', 2
A; Residues: 1-617, 'A', 619-703,'P', 705-792,'R', 794-1270,'S', 1272-1866,'G', 1868-2036,'N', 2
A; Molec: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
A; Molec: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanlmura, M.; Li, W.H.; Gotto Jr., A.M.
J. Biol. Chem. 261, 12918-12921, 1986
J. Millo: Sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA

A; Residues: 1-97, 'I', 99-328, 'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-

9-4132,'(G',4134-4180,'E', 4182-4563 <CHES.

A; Cross-references: GB: J02610; NID: 178803; PIDN: AAA35549.1; PID: g178804

A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides

A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides

A; Note: A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H

Proc. Natl. Acad. Sci. US.A. 38, 55048-5582, 1986

A; Reference number: A24320; MUID: 86287319; PMID: 3461454
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A Mesiduas: 1-97, I', 99-617, A', 619-941, YXIWSLPPKP, 951-1138, PTGRLPNCFSNGLICYSLWLHSFQE
A Mesiduas: 1-97, I', 99-617, A', 619-941, YXIWSLPPKP, 951-1138, PTGRLPNCFSNGLICYSLWLHSFQE
A Mesiduas: 1-97, I', 99-617, A', 109-91, A', 109-11, AAS1752.1, PID:9553189
B M. Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.W.; Sakaguchi, A.Y.; Naylor, Broc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A Mittle: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A Maccession: A24684
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A; Residues: 485-617, A', 619-1044 < LA2>
A; Residues: 485-617, A', 619-1044 < LA2>
A; Cross-references: GB:M12480; NID:g178792; PIDN:AAAS1751.1; PID:g178792
B; Procter, A.A.; Hardman, D.A.; Schilling, J.W.; Miller, J.; Appleby, V.; Chen, G.C.; Ki Proct. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr A; Reference number: A94088; MUID:86149325; PMID:3513177
A;IItle: Complete cDNA and derived protein sequence of human apolipoprotein B-100. A;Reference number: A93639; MUID:87016385; PMID:3763409
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;Residues: 1-291 <PRO>
;Cross-references: GB:M12681; NID:g17879; PIDN:AAA51753.1; PID:g178798

;Deeb, S. S.; Motulak; A.G.; Albers, J.J.

roc. Natl. Acad. Sci. U.S.A. 82, 4988-4986; 1985

;Title: A partial cDNA clone for human apoliprotein B.

;Reference number: A25774; MUID:85270450; PMID:3860836
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A; Note: this is a revision to the sequence from reference JH0101
R; Smith, T.J.; Hautamaa, D.; Maeda, N.
Refene 87, 309-310, 1990
A; Title: Sequence of the putative low-density lipoprotein receptor-binding regions of a R; Reference number: JH0101; MUID:90236327; PMID:2332175
A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein F;435-445/Region: receptor binding F;646-656/Region: receptor binding
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hypothetical 34.6 kD protein in arcB-gltB intergenic region - Escherichia coli (strain in Cispedies: Bscherichia coli
Cispedies: Bscherichia coli
Cispedies: Bscherichia coli
Cipate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
CiAccession: E65112
RiBlattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C. A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E65112
A;Accession: E65112
A;Accession: E65112
A;Accession: E65112
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A;Experimental source: strain K-12, substrain MG1655
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A;Gene: yhcC
C;Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ0486
                                                                                 Cispecies: Mesocricetus auratus (golden hamster)
Cipate: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
Rismith, T.J.
Aireasion: JH0102
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Pred. No. 2.3;
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Pred. No. 3.5;
2; Mismatches
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                                                          (fragment)
                                                   apolipoprotein B - golden hamster
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80.0%;
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Best Local Similarity 80.0
Matches 8; Conservative
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Matches 8; Conservative
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642 SRLTRKRGLK 651
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170 TQLARQRGLK 179
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AjRocession: B22010
AjRocession: B22010
AjRocession: B22011
AjRocession: B22012
AjRoce
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A;Accession: C60950
A;Accession: C60950
A;Molecule type: DNA
A;Residues: 1-269 <LANA
A;Cross-references: UNIPROT:Q60537; UNIPROT:Q60536
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
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                                                                                                              A,Title: Human apolipoprotein B: partial amino acid sequence A,Reference number: A22006, MUID:84208786, PMID:6373369
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80.0%; Pred. No. 1.3;
iive 2; Mismatches
                                                                                                                                                                                        A;Accession: A22006
A;Molecule type: protein
A;Residues: 873-892, K', 894-896 <LE1>
A;Accession: B22006
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R; Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
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3385 TRLTRKRGLK 3394
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216 SRLTRKRGLK 225
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Best Local Similarity
'-' 9; Conserve
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Best Local Similarity
Matches 8; Conserv
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Conserved hypothetical protein STY3508 [imported] - Salmonella enterica subsp. enterica sylvate: Itis species salmonella enterica subsp. enterica serovar Typhi Sylvate: Itis species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AH0906 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H., T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gara, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Hitle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov, A;Accession: AH0906
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N;Alternate names: starch (bacterial glycogen) synthase glgA
S;Species: Bacillus subtilis
C;Date: 19-Mar-1997 #sequence revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: 840051; E69632; 836627
R;Kiel, J.A.K.W.; Boels, J.W.; Beldman, G.; Venema, G.
A)OI. Microbiol. 11, 203-218, 1994
A;Title: Glycogen in Bacillus subtilis: molecular characterization of an operon encoding|
A;Reference number: 840048; MUID:94195107; PMID:8145641
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A;Residues: 1-484 <KIES
A;Redecule type: DNA
A;Residues: 1-484 <KIES
A;Residues: 1-484  
A;Residues: 1-484  
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C;Superfamily: Methanococcus jannaschli conserved hypothetical protein MJ0486
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Pred. No. 3.7;
2; Mismatches
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Best Local Similarity 70.0%;
Matches 7; Conservative ;
                                                      221 TSLTRKRGLK 230
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A;Molecule type: DNA
A;Residues: 1-309 <PAR>
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Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipate: 18-Jul-2001
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Cipate: 18-Jul-2001
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Cip
                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-309 <STO>
A;Cross-references: UNIPROT:P45476; GB:AE005174; NID:g12517832; PIDN:AAG58345.1; GSPDB:G
A;Experimental source: strain 0157:H7, substrain EDL933
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C.Species: Gallus gallus (chicken)
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C.Date: 31-Dec-1993 #sequence_revision of the apolipoprotein B domain that binds to the LDL A.Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A.Reference number: A60950; MUD:90324804; PMID:2373961
A.Accession: B60950
A.Residues: 1-275 <LAW>A.Residues: 1-275 <LAW>C.Supperfamily: apolipoprotein B C;Keywords: atheroselerosis; calcium; cholesterol metabolism: chulomirzon: alumination:
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;Residues: 1-275 cLAM>;
;Residues: 1-275 cLAM>;
;Reserences: UNIPROT:Q7LZ77
;Superfamily: apolipoprotein B
;Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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                   A,Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A,Reference number: A85480; MUD:21074935; PMID:11206551 A,Accession: B65985 A,Accession: B65985 A,Status: preliminary
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81.6%; Score 40; DB 2; Length 309;
Best Local Similarity 80.0%; Pred. No. 2.3;
Matches 8; Conservative 1; Mismatches 1; Indels
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Pred. No. 2.3;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 TOLARORGLK 179
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Best Local Similarity
Matches 8; Conserv
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us-09-823-418-6.rpr

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probable phosphoprotein phosphatase (EC 3.1.3.16) YBR0921 - yeast (Saccharomyces cerevi NyAlternate names: protein YBR0921; protein YBR125c C;Species Saccharomyces cerevisiae C;Species Saccharomyces cerevisiae C;Species Saccharomyces cerevisiae C;Date: 01-Aug-1995 #sequence revision 01-Sep-1995 #text_change 09-Jul-2004 C;Accession: S48288; S45993; S44703 R;Mannhaupt, G; Stucka, R; Ehnle, S; Vetter, I:; Feldmann, H. Yeast 10, 1363-1381, 1994 A;Title: Analysis of a 70 kb region on the right arm of yeast chromosome II. A;Reference number: S48285; MUID:95208357; PMID:7900426 A;Accession: S48288 A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                              A,Molecule type: DNA
A,Residues: 1.393 <MAN>
A,Cross-references: UNIPROT:P38089; EMBL:X78993; NID:g476045; PIDN:CAA55626.1; PID:g476
R,Fedmann, H.; Mannhaupt, G.; Schwarzlose, C.; Vetter, I.
submitted to the Protein Sequence Database, August 1994
A,Reference number: 845927
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0101; 833128; D60950
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
A;Title: Sequence of the putative low-density lipoprotein receptor-binding regions of agained mumber: JH0101; MUID:90236327; PMID:2332175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rilaw, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: D60950
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C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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A,Residues: 1-393 <FE2>
A,Residues: 1-393 <FE2>
A,Crose-references: EMBL:Z35994; NID:g536408; PID:g536409; MIPS:YBR125c
C,Genetics:
A,Gene: SGD:PTC4
A,Cross-references: SGD:S0000329
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C;Superfamily: human phosphoprotein phosphatase 1A
C;Keywords: phosphoric monoester hydrolase
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Pred. No. 29;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Molecule type: mRNA
A, Residues: 427-531,'S',533-700 <LAW>
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A;Molecule type: DNA
A;Residues: 1-531, DNA
A;Cross-references: EMBL:X15191
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Local Similarity 77.8%;
es 7; Conservative 1
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A, Accession: S33128
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A;Molecule type: DNA
A;Residues: 1-784 <SMI>
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Cydate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_cnange 09-001-2004
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Status: preliminary
A;Accession: B8361
A;Residues: 1-412 <STO>
A;Residues: 1-412 <STO>
A;Cross-references: UNIPROT:O9HVB8; GB:AE004882; GB:AE004091; NID:g9950919; PIDN:AAG0806
C;Genetics:
A;Gene: PA4677
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R.Law, A.; Scott, J.
Lipid Res. 31, 1109-1120, 1990
A.ithie: A cross-species comparison of the apolipoprotein B domain that binds to the LDL A.Reference number: A60950; MUID: 90324804; PMID: 2373961
A.Reference number: A60950
A.Residues: 1-274 < LAWA
Cross-references: UNIPROT: Q7M2U9
A.Roce: authors translated the codon GAT for residue 155 as His
C.Superfamily: apolipoprotein B
C.Superfamily: apolipoprotein B
C.Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                        A;Gene: glgA
A;Start codon: TTG
C;Superfamily: starch synthase
C;Keywords: glycogen/starch biosynthesis; glycosyltransferase; hexosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C,Species: Pseudomonas aeruginosa
C,Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A60950
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87.5%; Pred. No. 12;
iive 1; Mismatches
A;Experimental source: strain 168
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Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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dividroorotase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Accession: Ac2737
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Mocleil
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McCleil
R;Karp, P.; Romero, P.; Zhang, S.
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, Ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2737
A;Residues: Lajo «KUR»
A;Residues: Lajo «KUR»
A;Residues: Univers: Strain C58 (Dupont)
C;Genetics:
A;Genetics:
A;Genetics
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F;435-445/Region: receptor binding F;646-656/Region: receptor binding
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647 SRLMRKRGLK 656
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249 RIARORGVK 257
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                                                (without alignments)
98.508 Million cell updates/sec
                                          December 29, 2004, 12:13:11; Search time 58.4091 Seconds
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     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Q60537
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Q7UBF4
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GLGA BACCR
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Maximum Match 100%
Listing first 45 summaries
                              - protein search, using sw model
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Q13788
APB HUMAN
Q7Z600
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Q7YQM8
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Q7YR08
Q7TN64
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1: uniprot_sprot:*
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Maximum DB seq length: 2000000000
                                                                   US-09-823-418-6
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Match Length
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               Aas43926 bacillus
Aat3448 bacillus
P39125 bacillus th
Q6hc18 bacillus th
Q9fxm2 arabidopsis
Q818t0 arabidopsis
Q91va4 arabidopsis
Q91va4 arabidopsis
Q91vb8 pseudomas
Q93915 klebsiella
Q0528 lactobacill
Q7yqp1 crocuta cro
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   272yj6 bacillus
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Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotus.
NCBI_TaxID=57176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

MEDLINE=22761261; PubMed=12878460;

Amrino-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AF548396; AAP97352.1; -.
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Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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TISSUB-Liver;
TISSUB-2075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 414;
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1; Mismatches
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Pred. No. 0
972YJ6
AA543926
AAT34148
GLGA_BACSU
Q6HCTB
Q9PXM2
Q9PXM2
Q9LBTO
Q9LWA4
Q9LWA6
Q9JWBB
Q93915
Q7XQP1
Q8JLOGS28
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90.0%;
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258 TRLTRKRGLK 267
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 NCBI_TaxID=9541;
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B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
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SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.;
"The complete cDNA and amino acid sequence of human apolipoprotein B-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mahley R.W., Scott J., "Marting of Carboxyl-terminal domains, sites of gene expression, and chromosomal localization.";
Science 230:37-43(1985).
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MEDLINE-88300528; PubMed=2994255;
Knott T.J., Rall S.C., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priserley L.M., Robertson E., Rall L.B., Betsholtz C., Shows T.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 3056-3159 FROM N.A.
MEDLINE=666041888; PubMed=3903660;
Mentabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and characterization of RNA,";
                                                                                    MEDLINE=87016385; PubMed=3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181.
                                                                                                                                                                                                               SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE-888003974; Pubmed=3652907;
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C.,
Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
               Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Molecular cloning of human apolipoprotein B cDNA.";
Nucleic Acids Res. 13:8813-8826(1985).
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MEDILINE=85270450; PubMed=3860836;
Deeb S. Motullaky A.G. Albers J.J.;
"A partial cDNA clone for human apolipoprotein B Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
                                                                                                                                                                                Nucleic Acids Res. 14:7501-7503 (1986)
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MEDLINE=87041416; PubMed=3464946;
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                                                                      SEQUENCE FROM N.A.
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                                 NCBI_TaxID=9606
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MEDLINE=87191999; PubMed=2881086;

Carlsmon P., Darnfors C., Olofsson S.O., Bjursell G.;

Carlsmon P., Darnfors C., Olofsson S.O., Bjursell G.;

"Analysis of the human apolipoprotein B gene; complete structure of

Gene 49:29-51(1986).

FEMBL, MIS421, AAAS1758-11, -.

PIR; A27850, LPHUB.

GO: GO:0005376; C:extracellular; NAS.

GO: GO:0005319; F:lipid transporter activity; NAS.
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01-NOV-1986 (Rel. 03, Created)
01-NOV-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apollboprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein Name-APOS)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
metabolism in the cynomolgus monkey: evidence for post-
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Pred. No. 7.8;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                     the EMBL/GenBank/DDBJ databases
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596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
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Local Similarity 90.0%; Pred. No. 1.2;
les 9; Conservative 1; Mismatches
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                     transcriptional regulation.",
Biochim. Biophys. Acta 1086:326-334(1991)
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
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90.0%;
                                                                                                                                                  EMBL; X15737; CAA33755.1;
PIR; S32802; S32802.
                                                                                             TISSUE=Liver;
Murray R.;
Submitted (FEB-1992) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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Matches 9; Conservative
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Name=APOB;
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                                                                          SEQUENCE FROM N.A.
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                                      Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V., Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.; "Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L., "Sequence, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100.";
Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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                                                                                                                                                                                                                                                                                                                                                             PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDILINE=88018013; PubMed=3659919;
Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H.,
Silberman S.R., Cai S.-J., Dealypere J.P., Rosseneu M.,
Gotto A.M. Jr., Li W.-H., Chan L.;
"Apolipoproctein B-48 is the product of a messenger RNA with an organ-
specific in-frame stop codon.";
Science 238:363-366(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete protein sequence and identification of structural domains human apolipoprotein B."; Nature 323:734-738(1986).
                                                                                                                                                         [11]
SEQUENCE OF 1-1670 FROW N.A., AND VARIANT ILE-98.
MEDLINE-86287319; PubMed=3461454;
Protter A.A., Hardman D.A., Sato K.Y., Schilling J.W., Yamanaka M., Hort Y.J., Hjerrild K.A., Chen G.C., Kane J.P.;
"Analysis of CDNA clones encoding the entire B-26 region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr., Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R., Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
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Navajas M., Laurent A.-M., Moreel J.-F., Ragab A., Cambou J.-P., Cunny G., Cambien F., Roizes G.;
Detection by denaturing gradient gel electrophoresis of a new polymorphism in the apolipoprotein B gene.";
Hum. Genet. 86:91-93 (1990).
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Soria L.F., Ludwig E.H., Clarke H.R.G., Vega G.L., Grundy S.M.,
McCarthy B.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CALCIUM-BINDING DATA.
MEDLINE-86242245; PubMed=3087360;
Dashti N., Lee D.M., Mok T.;
"Apolipoprotein B is a calcium binding protein.";
Biochem. Biophys. Res. Commun. 137.493-499(1986).
                                                                                                                                                                                                                                                                                              apolipoprotein B.";
Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 83:1467-1471(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20143590; PubMed=10679026;
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                     MEDLINE=86149325; PubMed=3513177;
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SEQUENCE OF 1-291 FROM N.A.
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                                                                                                                apolipoprotein B.";
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FUNCTION: Apolipoprotein B is a major protein constituent of chylomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a French
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                                                                                                                                                                                          MEDINE=95190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
Hennilial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS SER-1914; ARG-1923; LEU-2739; ASP-3319; THR-3427; GLN-3432
AND ILE-3921.
                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97044521; PubMed=8889592;
Doriter O., Ricard S., Behague I., Souriau C., Evans A.E.,
Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
"Detection of new variants in the apolipoprotein B (Apo B) gene by
MEDLINE=91016974; PubMed=2216805;
Huang L.-S., Gavish D., Breslow J.L.;
"Sequence polymorphism in the human apoB gene at position 8344.";
Nucleic Acids Res. 18:5922-5922(1990).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AND LLE-3721.
MEDLINE-98141125; PubMed-9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 4563;
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 11;
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MEDLINE=97403938; PubMed=9259199;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutat. 10:160-163(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR-SSCP.";
Hum. Mutat. 8:282-285(1996).
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90.0%;
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Hum. Genet. 102:44-49(
                                                                                                                                                                      PDB CYS-3558
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Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AYZ43375; AAP50763.1; -.
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                                                                                            83.7%;
80.0%;
                                                                                                      Local Similarity 80.0
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279 SRLTRKRGLK 288
                                                                                                                                        1 TRLTRORGLK 10
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432
432 AA,
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436 4.
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                                  Lipoprotein.
NON TER
NON TER 43
SEQUENCE 432
                                                                                                                                                                                                                                                                                            Name=apoB-100
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SEQUENCE
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4polipoprotein B (Fragment)
61aucomys volans (Southern flying squirrel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Sciuridae, Petauristinae;
                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22761261; PubMed=12878460; Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.; Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.; An new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships."; Mol. Phylogenet. Evol. 28:225-240(2003).
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BEDIIMBE-275761261; PubMed=12878460;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolitopprotein B, provides compelling evidence for eutherian relationships.";
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Mammalla, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
NCBI_TaxID=9805;
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                                                                                                                                    Length 4563;
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Pred. No. 5.8;
2; Mismatches 0; Indels
                                                                                                         4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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EMBL, AY324608; AAP72970.1; -. GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:0006869; P:lipid transport; IEA. InterPro; IPR009454; DUF1081.
InterPro; IPR001747; Lipid_transprt_N. Pfam; PF06448; DUF1081; 1. SMART; SM0638; LPD_N; 1.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Diceros bicornis (Black Thinoceros).
                                                                                                                                  Score 45; DB 2;
Pred. No. 11;
1; Mismatches
                                                                                                                                                                                                                                                                  421 AA.
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90.0%;
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80.0%;
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Matches 8; Conservative
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264 SRLTRKRGLK 273
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                                                                                                                                Query Match
Best Local Similarity
Matches 9; Congery
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                                                                                                Lipoprotein.
SEQUENCE 49
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NON TER
NON TER 4
SEQUENCE 42
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MEDLINE-22761261; PubMed=12878460; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.; An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships "; Mol. Phylogenet. Evol. 28:225-240(2003).
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Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Nyctimene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker; apolipoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
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                                                                                                     Score 41; DB 2; Length 432;
Pred. No. 6;
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80.0%; Pred, No. 6.1;
iive 2; Mismatches 0; Indels
432
48171 MW; F27B7AB39604732C CRC64;
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48717 MW; 1C4A7EAD72D2C629 CRC64;
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyctimene albiventer (Common tube-nosed fruit bat).
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01-007-2003 (TrEMBLrel. 25, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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MEDLINE=22761261; PubMed=12878460;
Marine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; MY213169; AAPS0757-1;
InterPro: IPR00871; Beta lactanase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An ew phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AF548417; AAP97373.1; -.
                                                                                                                                                                                                                                                                                                                                                     Agoutí paca (Paca).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Agoutidae; Agouti.
NCBI_TaxID=108852;
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Mammalia, Eutheria, Rodentia, Hystricognathi, Hydrochaeridae,
                                 83.7%; Score 41; DB 2; Length 445; 80.0%; Pred. No. 6.2; ive 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83.7%; Score 41; DB 2; Length 445; 80.0%; Pred. No. 6.2; tive 2; Mismatches 0; Indels
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
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445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                 01-OCT-2003 (TrEMBLrel. 25, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Apolipoprotein B 100 (Fragment).
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            Query Match
Best Local Similarity 80.00,
Best Local Similarity
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                                                                                                                                      288 SRLTRKRGLK 297
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MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Mylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AX243383; AAP50771.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       Rousettus amplexicaudatus (Common rousette).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Chiroptera, Megachiroptera, Pteropodidae,
Pteropodinae, Rousettus.
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MEDLINE-2761261. PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for euchherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAPS0766.1; -.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi;
Mammalia, Eutheria, Edentata; Dasypodidae, Chaetophractus.
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                                                                                                 83.7%; Score 41; DB 2; Length 438;
80.0%; Pred. No. 6.1;
tive 2; Mismatches 0; Indels
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80.0%; Pred. No. 6.1;
1ive 2; Mismatches 0; Indels
                                                                   48734 MW; 2BD85BCBF4E2CC41 CRC64;
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Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                     438 AA.
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EMBL; AF548436; AAP97392.1;
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Best Local Similarity 80.00,
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Best Local Similarity 80.0
Matches 8; Conservative
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438 AA; 48FC
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281 SRLTRKRGLK 290
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281 SRLTRKRGLK 290
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438 AA;
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              Lipoprotein.
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MEDLINE=90236377; PubMed=2332175;

MEDLINE=90236377; PubMed=2332175;

A Smith T.J., Hautamaa D., Maeda N.;

"Sequence of the putative low-density lipoprotein receptor-binding T regions of apolipoprotein B in mouse and hamster.";

T regions of apolipoprotein B in mouse and hamster.";

Real, M35187; AAA37059.1; -.

R PIR; JOHO02; JH0102.

Lipoprotein.

In DODOROTER.

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10 NON TER.

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10 SEQÜENCE 780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
                                       Gaps
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SEQUENCE FROM N.A.
MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; Verbfill K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
evidence for eutherian relationships.";
MOI. Phylogenet. Evol. 28:225-240(2003).
EMBL; Ar243368; AAP50756.1; -.
                                                                                                                                                                                                                                                       Erethizon dormatum (North American porcupine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Erethizontidae,
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
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0
    DB 2; Length 445;
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Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches 0; Indels
                                  0; Indels
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445 AA; 49617 MW; 9572FESF5E7625F2 CRC64;
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780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     060536;
01-NOV-1996 (TrEWBLrel. 01, Created)
01-NOV-1996 (TrEWBLrel. 01, Last sequence update)
01-OCT-2003 (TrEWBLrel. 25, Last annotation update)
Hamster apolipoprotein (apoB) (Fragment).
Query Match
83.7%; Score 41; DB 5
Best Local Similarity 80.0%; Pred. No. 6.2;
Matches 8; Conservative 2; Mismatches
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288 SRLTRKRGLK 297
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NCBI_TaxID=10036;
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SEQUENCE 445
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Search completed: December 29, 2004, 12:37:33 Job time : 59.5202 secs

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December 29, 2004, 12:10:41 ; Search time 61.0227 Seconds (without alignments) 58.786 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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geneseqp2003a8;*
geneseqp2003b8;*
geneseqp20048;*
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49
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Apo-B100 Apo B bin Apo B 100 Apolipopr ApoB-100 Heparin b Human apo Nucleic a Peptide # Human liv Human apo Human apo Human Apo Apo B 100 Apo B 100 Human apo Human ali Human apo Nucleic a Apolipopr Amino aci Human apo Sequence Description Aay30689 Aaw57005 Aaw57205 Aaw57207 Aaw41261 Aaw96892 Abj 37575 Aaw57208 Aaw57208 Aaw57209 Aaw96876 Aaw64587 Aaw64587 Aaw64587 Abj 37687 Aaw52204 Aar72704 Aar72706 Aar72706 Aar72706 Aar72707 Aar72706 Aar72706 Aar72706 Aar72707 Aar72706 Aar72706 Aar72707 Aar727270 Aar727277 Aaw96826 Aau98981 BAdd48677 BAao15893 BAbr40253 B SUMMARIES AAR34031 ADJ57400 AAY31237 AAW96876 AAW64587 AAW96845 AAW57209 AAE14541 ABG52504 AAR72704 AAW57208 AAW41261 ABB37687 AAW41262 8 Query Match Length 3923 4536 4536 4560 4561 4563 4563 2463 Result No.

663 6 ABU79140 663 7 ADF43408 663 8 ADH18871 663 8 AD033445 663 8 AD033447 10 2 AAX30687 10 2 AAX30690 10 2 AAX30690 11 3 AAX30690 11 4 AAY30690 11 5 AAX30690 11 6 AAX30690 11 6 AAX30690		Aaw22911 Low densi Aap92302 Immunosup
	ABU79140 ADF4408 ADH18871 ADH18870 ADG33445 ADG33447 AAQ33184 AAX30687 AAX30687 AAX30686 AAW87217 AAW872173 AAW872173 AAW872173 AAW872173 AAW872173 AAW872173 AAW872173	AAW22911 AAP92302
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	00000000000000000000000000000000000000	4 4 5 4

ALIGNMENTS

RESULT 1

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate exheroselerosis. The peptides are derived from amino acids 3358 to 3367 of aposl10. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atheroselerosis, and in vivo assay methods for identifying compounds which modulate atheroselerosis and/or LDL-PG binding. They can Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Ŗ Claim 17; Page 57; 70pp; English. AAY30688 standard; peptide; 10 98US-0077618P. 99WO-US004805 Boren JOS; (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Innerarity TL, Homo sapiens WO9946598-A1 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 Synthetic AAY30688;

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Length 10; 0; Indels

Score 46; DB 2; Pred. No. 0.027; 1; Mismatches

93.9%;

9; Conservative

Query Match Best Local Similarity Matches 9; Conserv

Sequence 10 AA;

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1 TRLTEKRGLK 10 |||||:||||| TRLTDKRGLK 10

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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                            Gaps
                                                                                                                                                                                                                                                                          Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                      Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                    100.0%; Score 49; DB 2; Length 10; 100.0%; Pred. No. 0.0067; tive 0; Mismatches 0; Indels
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es 10; Conserv
                                                                  Sequence 10 AA;
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                                                                                                                                                                                                                                                                                                        Synthetic.
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Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.

Apo B binding site peptide 2.

03-AUG-1998 (first entry)

AAW57205;

AAW57205 standard, peptide, 11 AA.

RESULT 3

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKKKKKKK (1) or TTRLTRKKGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) crug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (11) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
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Pred. No. 0.074;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
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Best Local 8
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY10582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atheroscalerosis. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (FG). The method compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding wich disrupt LDL-PG binding without inhibiting LDL receptor binding such compounds can be used to atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulate atherosclerosis and in vivo assay methods for identifying compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the compounds which result in an increase in compounds without condition tends to stimulate or inhibit the formation of atherosclerotic lesions. Thus the assays may be used to determine whether compounds wind or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.

Claim 12; Page 52; 73pp; English.

Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing

4PI; 1999-551509/46.

Claim 17; Page 57; 70pp; English.

atherosclerosis.

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Baillie

Halbert GW, Owens MD,

WPI; 1998-230637/20.

(UYST) UNIV STRATHCLYDE

97WO-GB002610.

25-SEP-1997; 27-SEP-1996;

02-APR-1998

WO9813385-A2

Synthetic.

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Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                   (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 22; 60pp; English.
                                                 Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                            97WO-GB001255.
                                                                                                                                                                                                                                                                                                                                96GB-00009702,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89.88;
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              19-MAY-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Conservative
                                                                                                                    angiogenesis; cellular prothrombinase complex.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                      Bruckdorfer KR,
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                                                                                                                                                                                          Ношо варіелв
                                                                                                                                                                                                                                                                                              09-MAY-1997;
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                                                                                                                                                                                                                       WO9743311-A1
                                                                                                                                                                                                                                                           20-NOV-1997.
                                                                                                                                                                     Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-caturing, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least leptide component that has at least 1 binding site for an apo B protein creeptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least of invention are peptides containing an apo B binding sequence with at least of invention are peptides containing vectors for delivering an expectent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles are consistent apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                    Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
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Pred. No. 0.088;
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                                                                                                                                                                                                                                                                                                                                /note= "attached to retinoic acid"
                                                                                                                                                     Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                               AAW57207 standard; peptide; 13 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 13; Fig 7; 73pp; English.
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96GB-00020153
                                                                                                                  03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                              Modified-site
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                                                                                                                                                                                                                                                           Synthetic
                                                                                  AAW57207;
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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, insertions or substitutions, while retaining anti-coagulant properties of apolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-Z2 (I) X1 = S or (Y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 cc a. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated compositions or after surgery or in cases of heart attack, stroke etc.) and to inhibit angiogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits continuation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL;
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Pred. No. 0.1;
0; Mismatches 1; Indels
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Matches

RESULT 5 AAW41261

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20-JUL-2001; 2001US-0306726P
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                    (DXZO-)
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apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                 AAM96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (VLDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comporties LDL and inpoprotein a The apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, vivo or in vitro. for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardiovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatoid arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                              Composition comprising nucleic acid bound to LDL or VLDL lipoprotein -
used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                             Guevara JG, Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                            Claim 19; Fig 13D; 293pp; English.
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                                                                                                                                                                                    (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ37575 standard; peptide; 20
                                                                                                                             98WO-US011927
                                                                                                                                                   97US-00874807.
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                                                                                                                                                                                                                                      WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15 AA;
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                                                                                                                          10-JUN-1998;
                                                    Homo sapiens
                                                                                                                                                               14-MAY-1998;
                                                                         WO9856938-A1
                                                                                                                                                  13-JUN-1997;
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                                                                                                                                                                                                                                                                                         treatment.
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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                      Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Pred. No. 0.14;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "attached to cholesterol"
                                                Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW57208 standard; peptide; 22 AA.
                                                                                                                                                                 Disclosure; Fig 2; 79pp; English.
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                                        Hubbell JA, Schoenmakers R,
                                                                                                                                                                                                                                                                                                                                                     89.8%;
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                                                                                                                                     retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                         WPI; 2003-300420/29.
ETH ZUERICH
UNIV ZURICH
                                                                                                                                                                                                                                                                                                                                                                                                                                            7 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                      site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKKKHH (1) or TTRLTRKRGIK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete app B sequence, which is large and tends to aggregate, to provide binding
                                           sequence represents a specifically claimed Apo B 100 binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
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                                                                                                                                                                                                                                                                                                                                   0.15;
                                                                                                                                                                                                                                                                                                                                   Pred. No. 0.15
0; Mismatches
                                                                                                                                                                                                                                                       affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57209 Btandard; peptide; 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baillie G;
              Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97WO-GB002610.
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                                                                                                                                                                                                                                                                                                                                 90.06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                         16
                                                                                                                                                                                                                                                                                                                                                                            1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                     TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                       Sequence 22 AA;
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Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW57209;
                                                                                                                                                                                                                                                                                                                   Query Match
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

peptide binding to apo B protein delivering drugs to cancer cells

Non-natural lipid particle comprising receptor - useful as, e.g. vector for

WPI; 1998-230637/20.

that express this receptor.

Claim 13; Fig 7; 73pp; English.

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particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their useful as: (i) drug-targeting veceptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDE), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDE. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDE. In a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other cardiovascular diseases, and several other disorders such as periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                              .
0
                                                                                                                                                                                                                                                                                                                Score 44; DB 2; Length 22;
Pred. No. 0.15;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                89.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                      Local Similarity 90.0
les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       1 TRLTEKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLTRKGLK 16
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                                                                                                                                                                                                                                                                            Sequence 22 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide p62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE14541;
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                          Matches
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Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
                                                                                                                                                     Human apolipoprotein peptide fragment #1.
                                                                        AAW64587 standard, peptide, 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                    Moritz B, Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-416142/36.
                                                                                                                                                                                                                                                                                                                                                                            (IMMO ) IMMUNO AG.
                                                                                                                             23-OCT-1998
                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                         12-JAN-1998;
                                                                                                                                                                                                                                                                                               12-AUG-1998.
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                                                                                                  AAW64587;
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                                                                                                                                                                                                                                                                                                              Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                     Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                      Length 34;
                                                                                              1; Indels
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                                                                   Score 44; DB 5;
Pred. No. 0.24;
                                                                                            0; Mismatches
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                                                                                                                                                                                                        AAW96876 standard, peptide, 36 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                   89.88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-00874807.
98US-00079030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoogeveen RC,
                                                    Query Match
Best Local Similarity 90.00
Best Local 9; Conservative
                                                                                                                                                                                                                                                            22-APR-1999 (first entry)
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                   1 TRLTEKRGLK 10
                                                                                                                                          25 TRLTRKRGLK 34
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                                       Sequence 34 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                          W09856938-A1
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Schenk V;

Lang H,

98EP-00890007.

(first entry)

TRLTRKRGLK 20

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AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein in a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep coal trombosis), mutations in apolipoprotein (apo) genes (certain alledes of apoB indicates increased risk of developing Alzheimer's (associated with hypercypteinhaemia and venous thrombosis) and factor VII mutations (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. vhruses or prions. The method does not require complex apparatus for polymerase chain reactions, it is simple, standardisable and reliable and is protein a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
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                                                                                                                                        Example 2; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.8%;
90.0%;
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Best Local Similarity 90.00,
Best Local Similarity 90.00,
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AAW96845
ID AAW968
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1 TRLTEKRGLK 10

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                     Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, liver, cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%; Score 44; DB 4; Length 343; 90.0%; Pred. No. 2.6;
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                                                                                                                                                                                                                                                                                                                       Rank
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-020456F.
30-UTN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0033366.
21-SEP-2000; 2000US-023466PP.
27-SEP-2000; 2000US-023466PP.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                               (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                    2000US-0207456P.

2000US-00608408.

2000US-00632366.

2000US-0234687P.

2000US-0236359P.
                                                                                                                                                                                                                                                                                                                       Chen W,
                                                                             30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                       04-OCT-2000; 2000GB-00024263
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                                                                                                                                                                                                                                                                                                                     Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human liver peptide,
                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-483447/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
WO200157277-A2
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21-SEP-2000;
27-SEP-2000;
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                                     09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG52504;
                                                                                                                                                                                                                                                                                                                     Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (IDL), low density lipoproteins ((LDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of concers (particularly non-small cell lung carcinoma), diabetes, cystic
                                                                                                                                  Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinom; diabetes; arteriosclexosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89.8%; Score 44; DB 2; Length 51; 90.0%; Pred. No. 0.36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                              Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 16; Page 151; 293pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                             98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                        98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                   97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hoogeveen RC,
                                                      (first entry)
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TRLTRKRGLK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-070331/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51 AA;
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                             WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                           10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                        14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                        22-APR-1999
                                                                                                                                                                                                                                                                                                                   17-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                treatment.
                AAW96845;
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Best Loc Matches

RESULT 14 ABB37687

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XSXEXEXEXXXX

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Gaps

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1; Indels

(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR; Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult

[1Ver. comprishing one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver.

[2] May be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipporceinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABG47348-ABG5930 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification by the was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences

Sequence 343 AA;

Gaps ; 0 Query Match

89.8%; Score 44; DB 4; Length 343;
Best Local Similarity 90.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 1; Indels

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1 TRLTEKRGLK 10 ઠે

|||| ||||| 169 TRLTRKRGLK 178

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Search completed: December 29, 2004, 12:28:49 Job time : 61.0227 secs

us-09-823-418-7.rag

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-7 49

TRLTEKRGLK 10 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR 79: * 1: pir1: * 2: pir2: * 3: pir3: * 4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES -enoth DB ID Description	6 2 S32802 apolipop	1 LPHUB	2 C60950	779 2 JH0102 apolipoprotein B -	2 E60950 apolipopi	2 AI0767	2 A90985 hypotheti	2 D85830 hypothetical	2 C64970 hypothetical	2 S52148 amsK protein	2 S15296	E69580 arabinan-endo	2 S72953 probable	2 F87080	T41529	2 E82104 hypothetical	2 T01873 hypothetical	2 A60950	2 AG1306	2 C64119	2 JH0101	2 T01955 hypotheti	2 H84486 probable heli	F84517	2 D86481	2 T48965	2 I40540 verD protein	2 AF0336	Dronger and an analysis of the second
	 N		N	7	7	7	~	7	7		7	N	0	7	0	~	7	7			~	~	7		7	~		N	
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* Query Match	89.8	8.68		81.6		73.5	73.5	ω.	73.5	73.5	73.5	71.4	71.4	71.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	69.4	67.3	67.3	
Score	44	44	40	40	38	36	36	36	36	36	36	35	35	35	34	34	34	34	34	34	34	34	34	34	34	34	33	33	
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33 67.3 325 2 H69732 33 67.3 484 2 S40051 33 67.3 489 2 C86486 33 67.3 490 2 C86486 33 67.3 490 2 C86486 33 67.3 670 2 MOS129 67.3 1058 2 MOS129 67.3 1058 2 MOS139 32 65.3 125 1 ZHBT9 32 65.3 143 2 E9735 32 65.3 225 2 H7065 32 65.3 225 2 H7065 32 65.3 225 2 H7065 32 65.3 285 2 C83950	PBSX prophage ORF	protein F28J9.3 [i	starch synthase (E	protein F28J9.6 [i	hypothetical prote	hypothetical prote	DNA ligase (NAD) (apolipoprotein B -	gene 50 protein -	uncharacterized co	50S ribosomal prot	hypothetical prote	hypothetical prote	conserved hypothet	hypothetical prote	dipicolinate synth
	H69732	F86486	S40051	C86486	E71008	T05129	A40363	S65460	ZTBPT9	E97335	E90018	B64440	H70665	D82392	T27458	C83950
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ALIGNMENTS

RESULT 1

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apolipoprotein B - crab-eating macaque (fragment)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Oc-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 333802
R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchir Biochim. Japon Mulb:92075708; PMID:1742325
A;Reference number: S32802
A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-556 cPAP-
A;Cross-references: UNIPROT:Q28473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g9301
C;Superfamily: apolipoprotein B
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Pred. No. 0.86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%;
90.0%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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226 rkirkkicik 235 1 TRLTEKRGLK 10 셤 à

N; Contrains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C; Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A254452; I61909; I59510; I39474; I39469; I84624; I37179; PS0058
R; Ludwig, B.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sciona 6, 363-372, 1987 apolipoprotein B-100 precursor - human RESULT 2

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Asp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

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Accession: A29659
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A/MOCEGIAL Type: Type: mRNA
A/MOCEGIAL Type: Type: Type: Type: Typ
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A, Residues: 1-97, I', 99-328, 'V', 330-644,'I', 646-918,'P', 920-3318,'D', 3320-3426,'T', 3428-
4,132,'G',4134-4180,'E',4182-4563 -CHES
A, Cross-references: GB.J02610, NID: 9178803; PIDN: AAA35549.1; PID: 9178804
A, Note: a total of 236 residues were confirmed by direct sequencing of tryptic peptides
R, Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5682, 1986
A; Fitle: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A; Recence number: A24320; MUD: 86287319; PMID: 3461454
A; Recence number: A24320; MUD: 86287319; PMID: 3461454
A; Residues: 1-97,'I', 99-617,'A', 619-941,'YYIWSLPPKP', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A; Rossidues: 1-97,'I', JH OSPETCHARAY, AV.; ADICHARAS, A.Y.; 
                                                                                                                                                                                                       A; Molecule type: mRNA
A; Readdues: 1-272, N', 274-617,'A', 619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; Creaddues: 1-272,'N', 274-617,'A', 619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; Creaddues: 1-272,'N', 744506; NID:934330; PIDN:CAA28191.1; PID:934331
R; Law, S.W.; Grant, S.M.; H; Houchi, K.; Hoppattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 93, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Accession: A25267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-617, A', 619-703, 'P', 705-792, 'R', 794-1270, 'S', 1272-1866, 'G', 1868-2036, 'N', 2
4189-4220, 'M', 4222-4563 * LAW>
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
B; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M
A; Chen, S.H.; The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; MUID: 87008488; PMID: 3759943
                                   human apolipoprotein B-100,
A,Title: Complete cDNA and derived protein sequence of PA,Reference number: A93639; MUID:87016385; PMID:3763409 A,Accession: A25263
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Rishoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.; Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Reference number: A90084; MUID:86130855; PMID:3841481
A;Molecule type: mRNA
A;Molecule type: mRNA
B;Molecule type: MRNA
B;Molecule type: Molecule type: Mole
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A, Cost and Carlo Car
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Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990 A; Title: Isolation and characterization of Rulfhydryl and disulfide peptides of human ap A; Reference number: A35783; MUID:90319144; PMID:2115173 A; Contents: disulfide bonds
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A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
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A; Residues: 2129-2179, 2181-2235 <HA2>
A; Residues: 2129-2179, 2181-2235 <HA2>
A; Experimental securces: GB:MN8471
A; Experimental sources: intestine
A; Note: this mRNA from intestine includes a stop codon created by RNA editing in place
B; Mehrabian, M.; Schumaker, V.N.; Pareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner,
Nucleic Acids Res. 13, 6937-6953, 1985
A; Title: Human apolipoprotein B: identification of cDNA clones and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               stop codon in human intestine
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A,Residues: 3056-3159 cMEH>
A;Residues: 3056-3159 cMEH>
A;Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
R;Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.
Biochem. Biophys. Res. Commun. 148, 279-285, 1987
A;Title: Identification of a novel in-frame translational stop codon in
A;Reference number: A29659; MUID:88049670; PMID:2445342
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apolioprotein B - golden hamster (fragment)
Cispecies: Mesocricetus auratus (golden hamster)
Cispecies: Mesocricetus auratus (golden hamster)
Cispecies: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
CiAccession: JH0102
Ascession: JH0101
Asces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 40; DB 2;
Pred. No. 7.1;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P;435-445/Region: receptor binding P;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          81.6%;
80.0%;
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A,Gene: apoB
C,Superfamily: apolipoprotein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 80.0
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Best Local Similarity 80.0
Matches 8; Conservative
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642 SRLTRKRGLK 651
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Best Local 8
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                                                                                                                                                                                                A. Reterence number: A22006; MUID:84208786; PMID:6373369
A. Accession: A22006
A. Molecule type: protein
A. Rolecule type: protein
A. Residues: 3113. 'L'. 3115-3130,'R', 3132-3133,'P', 3135-3136,'R' cLE2>
A. Title: Structure of the human apolipoprotein B gene.
A. Reference number: A92564; MUID:87057153; PMID:2946672
A. Contents: annotation; gene structure
B. Riwagener, R.; Pfitzner, R.; Stoffel, W.
B. A. Title: Studies on the organization of the human apolipoprotein B 100 gene.
A. Reference number: A90715; MUID:87271140; PMID:2886136
A. Title: Studies on the organization of the human apolipoprotein B 100 gene.
A. Reference number: A90715; MUID:87271140; PMID:3301850
A. Title: Studies on the organization of the human apolipoprotein B 100 heparin binding sites.
A. Reference number: A90715; MUID:87281197; PMID:3301850
A. Title: Human apolipoprotein B-100 heparin binding protein.
B. Biol. Chem. 262, 11097-11103, 1987
A. Title: Apolipoprotein B-100 heparin binding protein.
A. Reference number: A90125; MUID:66242424; PMID:3081360
A. Contente annotein A. Mok, T.
B. Boothem: Biophys Res. Commun. 137, 493-499, 1986
A. Title: Apolipoprotein B a calcium binding protein.
A. Reference number: A90125; MUID:66242424; PMID:3081360
A. Contentes annoteiton; calcium binding protein.
A. Reference number: A901869
A. Title: Annotein A. Residence number: A901869
A. Reference numbe
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R, Lapid Res. 31, 1109-1120, 1990
A, Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI A, Reference number: A60950, MUID:90324804; PMID:2373961
A, Reference number: A60950, MUID:90324804; PMID:2373961
A, Rocession: C60950
A, Rolecus I-269 cLAW>
A, Residues: 1-269 cLAW>
A, Residues: 1-269 cLAW>
A, Cossiver references: UNIPROT:060537; UNIPROT:060536
C, Superfamily: apolipoprotein B
C, Reywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                 8
A:Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gарв
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Pred. No. 5.7;
0; Mismatches 1; Indel8
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                                                                                                                                 A;Title: Human apolipoprotein B: partial amino acid sequence. A;Reference number: A22006; MUID:84208786; PMID:6373369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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80.0%; Pred. No. 2.6;
iive 1; Mismatches
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Best Local Similarity 80.0
Matches 8; Conservative
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216 SRLTRKRGLK 225
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Best Local Similarity
Matches 9; Conserv
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apolipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: E60950
R;Law, A.; Scott, J.
J;Lipid Res. 31, 1109-1120, 1990
A;Ritler A cross-species comparison of the apolipoprotein B domain that binds to the LDI A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-275 < LAM>
A;Cross=rreferences: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
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Length 779;
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RESULT 4

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Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Escherichia coli

Cispecies: Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

Cispecies: C64970

Riblattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: C64970

A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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C;Species: Erwinia angles: Erwinia
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R;Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
R;Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
A): Microbiol. 5, 695-713, 1991
A;Title: Structure and sequence of the rfb (O antigen) gene cluster of Salmonella seroval A;Reference number: S15296; MUID:91260484; PMID:1710759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPROT: Q46638; EMBL: X77921; NID: 9600426; PIDN: CAA54889.1; PID: 96004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-406 <BLAT>
A;Cross-references: UNIPROT:P71243; GB:AE000295; GB:U00096; NID:g1788354; PIDN:AAC75105
A;Experimental source: strain K-12, substrain MG1655
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Pred. No. 25;
1; Mismatches 0; Indels
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Pred. No. 25;
1; Mismatches
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A;Molecule type: DWA
A;Residues: 1-411 <MOL>
A;Cross-references: UNIPROT: P26388
C;Keywords: transmembrane protein
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87.5%;
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87.5%;
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Best Local Similarity 87.5
ابت 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
               230 RLTEKKGL 237
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231 RLTEKKGL 238
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A;Residues: 1-407 <BU2>
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A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D8530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-406 <STO>
A;Cross-references: UNIPROT:Q8X7P5; GB:AE005174; NID:g12516235; PIDN:AAG57104.1; GSPDB:G C;Genetics: wcal
Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
Reference number: AB0502; MUID:21534947; PMID:11677608
Accession: A10767
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A;Experimental source: strain 0157:H7; substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cispecies: Escherichia coli
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipate: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
Cipacession: A90985
R.Hayachi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genc
A.Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein EC82849 [imported] - Escherichia coli (strain 0157:H7, substrain
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                                                                       A,Accession: A10767
A;Acture: preliminary
A;Molecule type: Dax
A;Residues: 1-406 < PAR>
A;Residues: 1-406 < PAR>
A;Cross-references: GB:AL513382; PIDN:CAD02463.1; PID:g16503330; GSPDB:GN00176
C;Genetics:
A;Gene: STY2310
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Pred. No. 25;
1; Mismatches 0; Indels
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Pred. No. 25;
1; Mismatches (
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1; Mismatches
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87.5%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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230 RLTEKKGL 237
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A; Map position: 3
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C;Species: Bacillus subtilis
C;Saccession: E65580
R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Garter, N.; Ebrich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
A;Ebrlich, S.D.; Emmerson, P.T.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A,Authors: Laubber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maudea, S.; Maucell, M.; Anthors: Laubber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Dohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A,Authors: Schleich, S.; Schroeter, R.; Scoffene, F.; Sekiguchi, J.; Sekwaka, A.; Seron akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamameto, H.; Yamameto, K.; Yata, K.; Yata, K.; Yoshida, R.; Reference number: A69580; MUID:99044033; PMID:9384377
A; Reference number: A69580; MUID:99044033; PMID:9384377
A; Reference number: A131 «KUN»
A; Roches Preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Reference number: MIDPAC, DAR, 20118. GR. 21.0013.
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C;Genetics:
C;Genetics:
C;Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongation C;Keywords: duplication; GTP binding; nucleotide binding; P-loop C;Keywords: duplication; GTP binding motif b homology <ETI>F;31-38/Region: uncleotide-binding motif A (P-loop)
F;31-38/Region: GTP-binding NKXD motif F;152-154/Region: GTP-binding SAK/L motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P94522; GB:Z99118; GB:AL009126; NID:g2635200; PIDN:CAB14841. A;Experimental source: strain 168 C;Genetics: A;Gene: abnA
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NiAlternate names: u0247e protein
C:Species: Mycobacterium leprae
C:Species: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
                                                                Gaps
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Length 411;
                                                                0; Indels
   DB 2;
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R; Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A; Description: Mycobacterium leprae cosmid L247.
A; Reference number: S72589
A; Accession: S72953
                             Pred. No. 25;
1; Mismatches
      Score 36;
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70.08;
73.5%;
87.5%;
                                Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
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TGLTEERGLR 68
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235 RLTEKKGL 242
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A,Molecule type: DNA
A,Residues: 1-461 <SMI>
   Query Match
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probable GTP-binding protein [imported] - Mycobacterium leprae
[Species: Mycobacterium leprae
[Spacession: F8708]
[Spacess
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C;Superfamily: Mycobacterium leprae probable GTP-binding protein; translation elongatio
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A;Molecule type: DNA
A;Residues: 1-199 < WOO>
A;Kesidues: 1-199 < WOO>
A;Cross-references: UNIPROT: Q9Y7V1; EMBL: AL049498; PIDN: CAB39908.1; GSPDB:GN00068; SPDB
A;Experimental source: strain 972h-; cosmid c645
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A;Residues: 1-462 <STO>
A;Cross-references: GB:AL450380; NID:g13093268; PIDN:CAC31753.1; GSPDB:GN00147
C;Genetics:
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F;198-319/Domain: translation elongation factor Tu homology <ET2>F;204-211/Region: nucleotide-binding motif A (P-loop)
F;316-319/Region: GTP-binding NKXD motif
F;349-351/Region: GTP-binding SAK/L motif
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Pred. No. 44;
1; Mismatches
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Best Local Similarity 77.8%;
Matches 7; Conservative
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les 7; Conservative
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Matches 7; Conservative
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452 RVREKRGLK 460
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TISSUE=Liver;
MEDLINE=92075708; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,
Marotti K.R., Melchior G.W.;
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NCBI_TaxID=9541;
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Q72600 homo sapien
Q7x10 dicers bic
Q7yqm8 nyctimene a
Q7yr04 rousettus a
Q7yr08 chaetophrac
Q7tn74 hydrochoeru
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Q7tn71 erethizon d
Q60536 mesocricetu
Q71277 gallus gall
Q71277 gallus gall
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Q7yqm9 cnnithorhym
Q7yqm0 tachyglossu
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Q6dcx0 xenopus lae
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Bac98516 oryza sat
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Actus vociferans (Spix's owl monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotinae; Aotue.
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MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
evidence for eutherian relationships.',
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AFS48396; AAP97352.1;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 24, Last annotation update)
Apolloportein B (Fragment)
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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               Q83kj4
Q7n1v8
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P26388
Q7acp5
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Q8E931
Q8E5h7
Q8E5h7
Q8E5h8
Q9E638
Q9E638
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Pred. No. 2.5;
0; Mismatches 1; Indels
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45955 MW; EEFA8492157E1BDE CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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              083KJ4
Q7N1V8
WCAL_ECOLI
WCAL_SALTY
Q7ACP5
Q7UCB6
Q8CB31
Q8Z5H7
Q8X7P5
Q8X7P5
AMSK ERWAM
Q9ARB8
PT17_STYPL
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90.0%;
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RTT REFERENCE REPORT OF FT REPORT REP

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                    NCBI_TaxID=9606;
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MEDLINE-87191999; PubMed=2883086;
Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.;
"Analysis of the human apolipoprotein B gene; complete structure of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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metabolism in the cynomolgus monkey: evidence for post-
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Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                     Length 596;
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                                                                                                                                Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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596 AA; 66757 MW; B13BBA74E25C3120 CRC64;
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GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport; NAS.
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                         transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991)
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90.08;
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Gene 49:29-31 (1986).
EMBL; M14421; AAA51758.1; -.
PIR; A27850; LPHUB.
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PIR; S32802; S32802.
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                                                                                         SEQUENCE FROM N.A.
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                                                                                                             TISSUE=Liver;
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OSSEEDTHAN

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"The complete sequence and structural analysis of human apolipoprotein B-100: relationship between apoB-100 and apoB-48 forms."; EMBO J. 5:3495-3507(1986).
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MEDLINE=85300528; PubMed=2994225;

Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
Priestley L.M., Robertson B., Rall L.B., Betsholtz C., Shows T.B.,
Mahley R.W., Scott J.;
"Human apolipoprotein B: structure of carboxyl-terminal domains, sites
of gene expression, and chromosomal localization.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND VARIANTS ILE-98 AND GLU-4181.
MEDLINE=87008488; PubMed=3759943;
Chen S.-H., Yang C.-Y., Chen P.-F., Setzer D., Tanimura M., Li W.-H.,
Gotto A.M. Jr., Chan L.,
anin and sequence of human apolipoprotein B-
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MEDLINE-86041888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
Kirchgesener T.G., Lin H.-C., Wang X., Ma Y., Mendiaz E., Lusis A.J.;
"Human apolipoprotein B: identification of cDNA clones and
characterization of mRNA.";
MEDLINE-87016385; PubMed-3763409;
Knott T.C., Wallis S.C., Powell L.M., Pease R.J., Lusis A.J.,
Blackhart B., McCarthy B.J., Mahley R.W., Levy-Wilson B., Scott J.;
"Complete cDNA and derived protein sequence of human apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [8] SEQUENCE OF 1937-2018 AND 3811-4334 FROM N.A., AND VARIANT GLU-4181. MEDLINE=86093680; PubMed=3841204; Carlsson P., Olofsson S.O., Bondjers G., Darnfors C., Wiklund O., Bjursell G.; "Molecular cloning of human apolipoprotein B cDNA."; Nucleic Acids Res. 13:8813-8826(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Law S.W., Grant S.M., Higuchi K., Hospattankar A.V., Lackner K.J., Lee N., Brewer H.B. Jr., Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino acid sequence.", Proc. Natl. Acad. Sci. U.S.A. 83:8142-8146(1986).
                                                                                                                                                                                                                                       [2]
SEQUENCE FROM N.A., AND VARIANT GLU-4181.
MEDLINE=88003974; PubMed=3652907.
Ludwig E.H., Blackhart B.D., Pierotti V.R., Caiati L., Fortier C Knott T., Scott J., Mahley R.W., Levy-Wilson B., McCarthy B.J.;
"DNA sequence of the human apolipoprotein B gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=87161758; PubMed=3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
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MEDLINE=88270450; PubMed=3860836;
Deeb S.S., Motulaky A.G., Albers J.J.;
"A partial cDNA clone for human apolipoprotein B
Proc. Natl. Acad. Sci. U.S.A. 82:4983-4986(1985)
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MEDLINE=87041416; PubMed=3464946;
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VARIANT LEU-2739.
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                      Protter A.A., Hardman D.A., Schilling J.W., Miller J., Appleby V., Chen G.C., Kirsher S.W., McEnroe G., Kane J.P.; "Isolation of a cDNA clone encoding the amino-terminal region of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang C.-Y., Chen S.-H., Gianturco S.H., Bradley W.A., Sparrow J.T., Tanimura M., Li W.-H., Sparrow D.A., Deloof H., Rosseneu M., Lee F.-S., Gu Z.-W., Gotto A.M. Jr., Chan L.; "Sequence, structure, receptor-binding domains and internal repeats of human apolipoprotein B-100.";
Nature 323:738-742(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Association between a specific apolipoprotein B mutation and familial defective apolipoprotein B-100."; Proc. Natl. Acad. Sci. U.S.A. 86:587-591(1989).
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                                                                                                                                                                                                                            MEDLINE=88818019; PubMed=3659919; Chen S.-H., Habib G., Yang C.-H., Gu Z.-W., Lee B.R., Weng S.-H., Silberman S.R., Cai S.-J., Deelypere J.P., Rosseneu M., Gotto A.M. Jr., Li W.-H., Chan L.; Gablipoprotein B48 is the product of a messenger RNA with an organspecific in-frame stop codon.";
                                                                                                                                                                                                                                                                                                                                                     MEDLINE-87039351; PubMed=3773997;
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Innerarity T.L., Blackhart B., Taylor W.R., Marcel Y., Milne R.,
Johnson D., Fuller M., Lusis A.J., McCarthy B.J., Mahley R.W.,
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                                                                                                    SEQUENCE OF 1-1670 FROM N.A., AND VARIANT ILE-98.
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polymorphism in the apolipoprotein B gene.";
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                                                               apolipoprotein B.";
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                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 83:5678-5682(1986)
                                                                                                                                                                                                                 PARTIAL SEQUENCE, AND IDENTIFICATION OF APO-B48.
MEDLINE=88018019; PubMed=3659919;
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            MEDLINE=86149325; PubMed=3513177;
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                                                                                                                                                                                                                                                                                                              Science 238:363-366(1987).
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Rabes J.P., Varret M., Saint-Jore B., Erlich D., Jondeau G., Krempf M., Girandet P., Junien C., Boilau C.; "Familial ligand-defective apolipoprotein B-100: simultaneous detection of the ARG3500--SGLN and ARG3531---CYS mutations in a French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Apolipoprotein B is a major protein constituent of rehlomicrons (apo B-48), LDL (apo B-100) and VLDL (apo B-100). Apo B-100 functions as a recognition signal for the cellular binding and internalization of LDL particles by the apoB/E receptor.
                                                                                                                                                                                              MEDLINE=95190020; PubMed=7883971;
Pullinger C.R., Hennessy L.K., Chatterton J.E., Liu W., Love J.A., Mendel C.M., Frost P.H., Malloy M.J., Schumaker V.N., Kane J.P.;
"Familial ligand-defective apolipoprotein B. Identification of a new mutation that decreases LDL receptor binding affinity.";
J. Clin. Invest. 95:1225-1234(1995).
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MEDLINE-9811125; PubMed=9490296;
Leren T.P., Bakken K.S., Hoel V., Hjermann I., Berg K.;
"Screening for mutations of the apolipoprotein B gene causing
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANTS LEU-1437; SER-1914; LYS-2566; THR-3121; ALA-3945; MET-4128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97044521; PubMed=8889592;
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Arveiler D., Marques-Vidal P., Luc G., Roizes G., Cambien F.;
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                  Huang L.-S., Gavish D., Breslow J.L.; "Sequence polymorphism in the human apoB gene at position 8344."; Nucleic Acids Res. 18:5922-5922(1990).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 28;
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MEDLINE-97403938; PubMed-9259199;
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MEDLINE=91016974; PubMed=2216805;
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Hum. Mutat. 8:282-285(1996).
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(TrEMBLrel. 25, I
(TrEMBLrel. 26, I
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Hum. Genet. 102:44-49
                                                                                                                                                                        VARIANT FDB CYS-3558.
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Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AY243375; AAP50763.1; -.
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                                                                                      Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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432
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Matches
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Mammalia, Eutheria, Rodentia, Sciurognathi, Sciuridae, Petauristinae,
                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22761261; PubMed-12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for euherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
Diceros bicornis (Black rhinoceros).
Bukaryotes, Netazza, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
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                                                                                                                                     Length 4563;
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                                                                                                          4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
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46747 MW; D47B77BD4F864FD1 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
          GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:006669; P:lipid transport; IEA. InterPro; IPR009454; DUF1081. InterPro; IPR001474; Lipid_transprt_N. Pfam; PF06448; DUF1081; 1. Pfam; PF0147; Vitellogenin_N; 1.
                                                                                                                                    Score 44; DB 2;
Pred. No. 28;
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EMBL; AY324608; AAP72970.1; -.
                                                                                                                                   89.8%;
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80.0%;
                                                                               SMART; SMOO638; LPD N; 1.
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Matches 8; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                              Lipoprotein.
SEQUENCE 4:
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SEQUENCE
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SEQUENCE FROM N.A.

MEDLINE=22761261; PubMed=12878460;

Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Am new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

"I newloaenet. Evol. 28:225-240(2003).
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Nyctimene albiventer (Common tube-nosed fruit bat).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;

Pteropodinae; Nyctimene.
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MEDLINE=22761261; PubMed=12878460;
MEDLINE=22761261; PubMed=12878460;
Mayne R.K., Springer M.S.;
Maine-Madeon H., Koepfil K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;
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                                                          81.6%; Score 40; DB 2; Length 432;
80.0%; Pred. No. 18;
tive 1; Mismatches 1; Indels
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432 AA; 48171 MW; F27B7AB39604732C CRC64;
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436 436
436 AA; 48717 MW; 1C4A7EAD72D2C629 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment)
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker; apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Bvol. 28:225-240(2003).
EMBL; AR243369; AAPS0757-11.
InterPro; IPR00871; Beta lactanase A.
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

MEDLINES-2761261, PubMed=12878460;

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AFS48417; AAP97373.1; -.
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Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Hydrochaeridae;
                                                                                                                                                                                                                                                                                                                                                 Agouti paca (Paca).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Hystricognathi, Agoutidae, Agouti.
NCBI_TaxID=108852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81.6%; Score 40; DB 2; Length 445; 80.0%; Pred. No. 18; tive 1; Mismatches 1; Indels
                                Score 40; DB 2; Length 445; Pred. No. 18;
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445 445
445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
445 AA; 49564 MW; 2DA5DC3ED2F0FDD2 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2004 (TEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment).
                                                                                                                                                                                                                                                          01-00T-2003 (TrEMBLrel. 25, Created)
01-00T-2003 (TrEMBLrel. 25, Last sequence update)
01-00T-2003 (TrEMBLrel. 25, Last annotation update)
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                                81.6%;
80.0%;
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Query Match

Best Local Similarity 80.00.
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                                                                                                                                        288 SRLTRKRGLK 297
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Rousettus amplexicaudatus (Common rousette).
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Chiroptera; Megachiroptera; Pteropodidae;
Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AX243383; AAP50771.1; -.
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BEDLINE-2761261, PubMed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243378; AAPS0766.1; -.
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Chaetophractus villosus (South American armadillo).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Edentata, Dasypodidae, Chaetophractus.
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                                                                                                     Score 40; DB 2; Length 438;
Pred. No. 18;
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438 438
438 AA, 48597 MW, 41C890DEAF95C872 CRC64;
                                                                   438 AA; 48734 MW; 2BD85BCBF4E2CC41 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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 EMBL; AF548436; AAP97392.1;
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281 SRLTRKRGLK 290
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MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

MEDLINE=90236327; PubMed=2332175;

Maeda N.;

"Sequence of the putative low-density lipoprotein receptor-binding regions of apolipoprotein B in mouse and hamster.";

Gene 87:309-310(1990).

EMBL; M35187; AAA37059.1; -.

PIR; C60950; C60950.

PIR; JH0102; JH0102.
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MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243368; AAP50756.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brethizon dorsatum (North American porcupine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Hystricognathi, Erethizontidae;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hamster apolipoprotein (apol) (Fragment).
Mesocricetus auratus (Golden hamster).
Mesocricetus (Bordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae, 11 Exidentia (Tricetinae).
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Query Match

81.6%; Score 40; DB 2; Length 445;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Indels
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81.6%; Score 40; DB 2; Length 445;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 1; Mismatches 1; Indels
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445 AA; 49617 MW; 9572FESF5E7625F2 CRC64;
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780 780
780 AA; 86625 MW; E371D1B2079D8F7E CRC64;
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1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B (Fragment).
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288 SRLTRKRGLK 297
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288 SRLTRKRGLK 297
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   81.6%; Score 40; DB 2; Length 780;
80.0%; Pred. No. 32;
iive 1; Mismatches 1; Indels
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Query Match
Best Local Similarity 80.0
Matches 8; Conservative
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1 TRLTEKRGLK 10

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Search completed: December 29, 2004, 12:37:34 Job time : 59.5202 secs

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December 29, 2004, 12:10:41; Search time 61.027 Seconds (without alignments) 58.786 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Aay30689 Apo-B100		-	Aaw57207 Apo B 100		Aaw96892 ApoB-100	Abj37575 Heparin b	-	Aaw57209 Apo B 100	Aae14541 Human apo	Aaw96876 Nucleic a	Aaw64587 Human apo		Abb37687 Peptide #			Aar34031 Sequence	0	Aay31237 Human Apo	2 Apolip	Aaw96826 Amino aci	Aau98981 Human apo	Add48677 Human Pro	Aao15893 Human apo	Abr40253 Human ali
SUMMARIES	AAY30689	AAY30688	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504	AAR72704	AAR34031	ADJ57400	AAY31237	AAW41262	AAW96826	AAU98981	ADD48677	AA015893	ABR40253
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% Query Match	100.0	92.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0	84.0
Score	50	46	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
Result No.		7	٣	4	2	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abu79140 Apolipopr Add1498 Apolipopr Add18871 Human apo Add3345 Human apo Add3345 Human apo Add3345 Human apo Add3345 Human apo Add33469 Apo-B100 Aag57562 Arabidops Aag57562 Arabidops Aag5914 Arabidops Aag5914 Arabidops Aag59301 Arabidops Aag59301 Arabidops Aag59301 Arabidops Aay30682 Apo-B100 Aay30682 Apo-B100 Aay30692 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100 Aay30696 Apo-B100	, ,			a proteoglycan receptor mutation.	n; atherosclerosis; LDL; atherosclerotic lesion.									ing of low density lipoprotein ning compounds for reducing		**Tagnon represent apo-Bloo derived peptides showing proteoglycan mutations. They were created to identify compounds which atherosclerosis. The peptides are derived from amino acids 3158 of apoBloo. The method comprises detecting compounds which affect sity lipoprotein (LDL) binding with proteoglycan (PG). The method inhibiting LDL receptor binding. Such compounds can be used to revent the formation of atherosclerotic lesions and prevent prevent the formation of atherosclerotic lesions and prevent human apo-Bloo can be used as an in vivo model system for the atherosclerosis, and in vivo assay methods for identifying such modulate atherosclerosis and/or LDL-PG binding. They can
ABU79140 ADH18871 ADH18871 ADH18871 ADH33445 AD033445 AAX36659 AAX36659 AAX3669 AAX30690 AAX30687 AAX30687 AAX30687 AAX30687 AAX30687 AAX30687 AAX30687 AAX30687 AAX30687		10 AA.		showing a prote	eceptor mutation; at proteoglycan; LDL;									affect binding c e.g. obtaining	English.	ement apo-B100 derive They were created to osis. The peptides are the method comprises tin (LDL) binding with teceptor binding. The receptor binding. The formation of athero transgenic non-human of can be used as an osis, and in vivo assis, and in vivo assis.
らて800004cmmmmmmacacacacacacacacacacacacacacacac			ç	sho	receptor ; proteo				808	18P					Eng	wer wer Thur Thur Thur Thur Thur Thur Thur Thu
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		; peptide;	st entry)	peptide	teoglycan re ipoprotein;				99WO-US004805	98US-0077618	CALIFORNIA.	Boren JOS	. 94	inds whi	, 70pp;	wutations. They we mutations. They we atherosclerosis. I atherosclerosis. It illustrates the metty lipoprotein (Litter for identifying unhibiting LDL receiptores. The transcuman apo-B100 can atherosclerosis, which modulate at
000000000000000000000000000000000000000	•	standard;	(first	ved 1	eog God				166	186	T I	ĕ	509/4	mpou can,	57	1 operations of the control of the c
8 8 8 8 8 8 8 6 7 7 7 7 7 7 7 7 7 7 7 7	•	and		riv	11.	œ.						ŢĽ,	515	gly ogi	Page	30700 untation there apos apos apos apos apos apos apos apos
6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		0689	7-NOV-1999	Apo-B100 deri	Apo-B100; prot low density li	Synthetic. Homo sapiens	WO9946598-A1	16-SEP-1999	5-MAR-1999	10-MAR-1998	GC) UNIV	rarity	; 1999-5	Identifying compounds which with proteoglycan, used for, atherosclerosis.	Claim 17; Po	1) 10 10 10 10 10 10 10 10 10 10 10 10 10
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT 1	XX AAY	XX DT 17-	XX DE Apo	KW Apo	OS Synth	PN WO9	PD 16-	PF 05-	PR 10-	PA (REGC	PI Inn	DR WPI;	PT Ide PT wit PT ath	PS Cla	CC ANY3 CC Trece CC T

us-09-823-418-8.rag

Sequence 10 AA;

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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                       Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                              ;
                                                                                                   100.0%; Score 50; DB 2; Length 10; 100.0%; Pred. No. 0.0029; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                            AAY30688 standard, peptide, 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US004805
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                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                           Conservative
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                                                                                                                                                 TRLIDKRGLK 10
                                                                                                                                                              1 TRLTDKRGLK 10
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                                                                                                   Query Match
Best Local Similarity
                                                                               Sequence 10 AA;
                                                                                                                                                                                                                                                                            17-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                         Synthetic
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Matches
                                                                                                                                                                                                                    AAY30688
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteeglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which compounds the method comprises detecting compounds which affect to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteeglycan (FG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as an in vivo model system for the express human apo-B100 can be used as in vivo assay methods for identifying compounds which result in an increase in a labo be used to identify compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
Claim 17; Page 57; 70pp; English.
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84.0%; Score 42; DB 2; Length 11; 90.0%; Pred. No. 0.14; 1.1ve 0; Mismatches 1; Indels

Conservative

Local Similarity

Query Match Best Loc Matches 1 TRLIDKRGLK 10

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2 TRLTRKRGLK

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) that express an apo B protein receptor, and (ii) additives for cells culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                                      Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide binding to apo B protein delivering drugs to cancer cells
                                       Gape
                                       ö
        Length 10;
                                      Indels
                                      .
0
      Score 46; DB 2;
Pred. No. 0.019;
                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Non-natural lipid particle comprising receptor - useful as, e.g. vector for that express this receptor.
                                                                                                                                                                         AAW57205 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 52; 73pp; English.
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                                                                                                                                                                                                                                                                        Apo B binding site peptide 2.
      92.0%;
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Query Match
Best Local Similarity 90.0
Matches 9, Conservative
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1 TRLTEKRGLK 10
                                                                  1 TRLIDKRGLK 10
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                                                                                                                                                                                                                                                                                                                                                                                                     WO9813385-A2
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                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                          AAW57205;
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This sequence is an example of the peptide of the invention. It has the formula (I), or their variants with one or more internal deletions, consecuted insertions or substitutions, while retaining anti-coagulant properties of appolipoprotein B-100 (apoB-100). Z1-KAQ-X1-KKNKHRHS-X2-T-ZZ (I) X1 = S or C y; X2 = T or I; Z1 = the N terminus of the peptide, or 1-47 amino acids (aa); Z2 = the C terminus of the peptide, a terminal amide group or 1-77 or a. Compositions containing the peptide are used for simultaneous, separate or sequential treatment of cancer, particularly to prevent metastatic spread. They are also used to inhibit thromboplastin-mediated conting or after surgery or in cases of heart attack, stroke etc.) and to inhibit anglogenesis, cellular differentiation or apoptosis. KRAD-14, which is active as such or as part of a 98-aa peptide, inhibits continuation of the prothrombinase complex; and prevents activation of the prothrombinase complex; and prevents activation of factor VII on the surface of thromboplastin and of platelets by thrombin. It binds to the residues 58-66 of thromboplastin. Since (I) are much constitution or the residues of the more quickly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.
                                                                                                           Anti-coagulant; apolipoprotein B-100; apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; angiogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNLO ) ROYAL FREE HOSPITAL SCHOOL MED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure, Page 22, 60pp, English.
                                                                 Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%;
90.0%;
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                       (first entry)
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                                                                                                                                                                               prothrombinase complex
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15 AA;
                       19-MAY-1998
                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                         WO9743311-A1
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                                                                                                                                                                                                                          Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-taxgeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding
                                                                                                                                                                                                                                        Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells
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Pred. No. 0.16;
0; Mismatches 1; Indels
                                                                                                                                                                                                Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baillie G;
                                                               AAW57207 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97WO-GB002610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         that express this receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYST ) UNIV STRATHCLYDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TRLTDKRGLK 10
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Best Local Similarity
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Modified-site
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
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                                      Gaps
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                                      ö
  Length 15;
                                    1; Indels
Score 42; DB 2;
Pred. No. 0.19;
0; Mismatches
                                                                                                                                                                                                                  AAW96892 standard; peptide; 15 AA.
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AAW41261 standard; peptide; 15 AA.

RESULT 5 AAW41261

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Matches

AAW41261;

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20-JUL-2001; 2001US-0306726P.
                                                                                  Hubbell JA, Schoenmakers R,
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                                                                                                                WPI; 2003-300420/29.
                                      ETH ZUERICH
UNIV ZURICH
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                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                      Sequence 20 AA;
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Modified-site
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(UYZU-) 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      셤
                                                                                                                                                                                                                                                                                                                                                                                                 AAW96878-97 represent nuclear localisation signal sequence derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (LDL), and lipoprotein a. The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and apolipoproteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic
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apolipoprotein, binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CytoBtatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological; cardlovascular; circulatory; ligand; sulphated; sulphonated; tumour; rheumatold arthritis; hypoxia; diabetic retinopathy; heparin.
                                                                                                                                                                                                                                                                                                               Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84.0%; Score 42; DB 2; Length 15; 90.0%; Pred. No. 0.19; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                          Hoogeveen RC, Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heparin binding peptide sequence #28.
                                                                                                                                                                                                                                                                                                                                                                            Claim 19; Fig 13D; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABJ37575 standard; peptide; 20 AA.
                                                                                                                                                                                                                         (BAYU ) BAYLOR COLLEGE MEDICINE,
                                                                                                                                                                                 97US-00874807.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JUL-2002; 2002WO-US023419.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
                                                                                                                                                                                                                                                                                      WPI; 1999-070331/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 9, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2003007689-A2
                                                                                        WO9856938-A1
                                                                                                                                                   10-JUN-1998;
                                                                                                                                                                               13-JUN-1997;
14-MAY-1998;
                                                              Homo sapiens
                                                                                                                    17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
                                                                                                                                                                                                                                                        Guevara JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABJ37575;
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The invention relates to a novel ligand for binding a target biomolecule, which comprises a peptide having at least one sulphated or sulphonated amino acid and at least one amino acid chosen from neutral and positively charged amino acids. The novel ligands can be used for the treatment of e.g. tumours, rheumatoid arthritis, diabetic retinopathy and hypoxia. This sequence represents a heparin binding peptide relating to the
                                                                                                                                Use of a ligand comprising of at least one sulfated or sulfonated amino acid for the treatment of e.g. tumors, rheumatoid arthritis, diabetic retinopathy and hypoxia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "attached to cholesterol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.0%; Score 42; DB 6;
llarity 90.0%; Pred. No. 0.26;
Conservative 0; Mismatches
Maynard HD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW57208 standard, peptide, 22 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                Disclosure; Fig 2; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baillie
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particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human apoB-100 derived peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE14541 standard; peptide; 34 AA.
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                               Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAE14541;
                                                                                                                                                                                                                                                                                                                    Query Match
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        8888888888888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer calls that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding affinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo 8100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo B 100 binding site peptide analogue peptide D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.28
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                            84.0%; Score 42; 90.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW57209 standard; peptide; 22 AA.
                            Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLTDKRGLK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||| || ||||
TRLTRKRGLK 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 22 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW57209;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Gaps

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1; Indels

84.0%; Score 42; DB 2; Length 22; 90.0%; Pred. No. 0.28;

0; Mismatches

1 TRLIDKRGLK 10 7 TRLTRKGLK (first entry)

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The invention relates to peptides having affinity for oxidised low density lipoprotein (oxLDL), in cyclised or multimeric form. The peptide is useful in an immunoassay to determine the presence, and optionally, the amount of antibodies in a sample, having affinity for oxLDL. Preferably immobilised peptide is useful for measuring the amount of autoantibodies for oxLDL in a sample, especially a serum or plasma sample from a patient for evaluating the risk of coronary heart diseases, other periaortitis, pre-eclampsia, non-insulin-dependent diabetes and endothelial dysfunction. The peptide of the invention is stable, can be synthesised easily without the need to isolate proteins from a patient's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide useful in enzyme immunoassays for detecting oxidized low density lipoprotein which is a marker of coronary heart disease and other cardiovascular diseases, has affinity for oxidized low density
Oxidised low density lipoprotein; oxLDL; immunoassay; periaortitis; cardiovascular disease; coronary heart disease; pre-eclampsia; non-insulin-dependent diabetes; endothelial dysfunction; human; apoB-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 5; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-JUL-2000; 2000GB-00017641.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2001; 2001WO-GB003212.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARKT-) ARK THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Narvanen O, Yla-Herttuala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-179777/23
                                                                                                                                                                                                                                                                                                                                 WO200206314-A2.
                                                                                                                                                                                                                                      Ното варіеля
                                                                                                                                                    peptide p62.
                                                                                                                                                                                                                                                                                                                                                                                                                            24-JAN-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lipoprotein.
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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL)

Claim 13; Fig 7; 73pp; English.

that express this receptor.

Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells

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Baillie

Owens MD,

Halbert GW,

WPI; 1998-230637/20.

(UYST) UNIV STRATHCLYDE.

97WO-GB002610. 96GB-00020153

25-SEP-1997; 27-SEP-1996;

WO9813385-A2

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20

11 TRLTRKRGLK

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RESULT 12

AAW64587

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM96827-77 represent nucleic acid binding domains derived from human apolipoprotein B-100 (apoB-100). ApoB-100 is a major apoprotein component of very-low density lipoproteins (VLDL), intermediate density lipoproteins (ILDL) and lipoprotein a. The present sequence can be used in the composition of the invention. The present apporteins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense molecule (or ribozyme). Specifically they are used for gene therapy of cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
blood, and has a long half-life. The present sequence is human apoB-100 derived peptide p62 used in the invention
                                                                                                                    Gaps
                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                 Nucleic acid binding domain from apoB-100, residues 3348-3390.
                                                                                    Length 34;
                                                                                                                  1; Indels
                                                                                   DB 5;
                                                                                                0.45;
                                                                               Score 42; DB 5
Pred. No. 0.45;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Moore JP;
                                                                                                                                                                                                                                                       AAW96876 standard; peptide; 36 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16, Fig 12C, 293pp, English.
                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                               84.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-00079030.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US011927.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97US-00874807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoogeveen RC,
                                                                                                                                                                                                                                                                                                                   22-APR-1999 (first entry)
                                                                                                               9; Conservative
                                                                                                                                             1 TRLIDKRGLK 10
                                                                                                                                                                            34
                                                                                                                                                                           25 TRLTRKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-070331/06.
                                                                            Query Match
Best Local Similarity
                                                 Sequence 34 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 36 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9856938-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment.
                                                                                                                                                                                                                                                                                     AAW96876;
                                                                                                           Matches
                                                                                                                                                                                                                         RESULT 11
                                                                                                                                                                                                                                           AAW96876
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AAW64587 and AAW64588 are fragments of human apolipoprotein which are used with Factor V protein fragments in a novel method to detect the presence of a mutated protein. In a sample that may also contain the corresponding wild-type protein. The method is used to detect mutations that alter protein functions (either point mutation or small insertions or deletions), particularly in proteins involved in blood coagulation or metabolism of fat. Protein functions which are specially detectable are the Leyden mutation in factor V (associated with increased risk of deep vein thrombosis), mutations in apolipoprotein (apo) genes (certain allelse of apol indicates increased risk of developing Alzheimer's disease), thermostable 5.10-methylenetetrahydrofolate reductase (associated with increased risk of cardiovascular disease). The method can also be applied to proteins from pathogens, e.g. viruses or prions. The method does not require complex apparatus for polymerase complex apparatus for polymerase contribers and reliable and is particularly suited to routine screening. It also allows mutant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting or quantifying mutant protein in presence of wild-type protein comprises reaction with ligand - used to detect mutant blood coagulation factors or apolipoproteins for diagnosing risk of thrombosis.
                                                                                                                                    Factor V; human; detection; protein function; blood coagulation; apo; fat metabolism; Leyden mutation; deep vein thrombosis; apolipoprotein; Alzheimer's disease; 5,10-methylenetetrahydrofolate reductase; prion; hypercysteinaemia; factor VII; cardiovascular disease; pathogen; virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 0.49;
0; Mismatches 1; Indels
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                                                                                                      Human apolipoprotein peptide fragment #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Schenk V;
AAW64587 standard; peptide; 37 AA.
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AAW96845
ID AAW96845 standard; peptide; 51 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; Page 9; 18pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Lang H,
                                                                                                                                                                                                                                                                                                                                    98EP-00890007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in a sample to be quantified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%;
90.0%;
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 90.0
-2.0
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Moritz B, Kiessig S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-416142/36.
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TRLTRKRGLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 37 AA;
                                                                   23-OCT-1998
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  12-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                     13-JAN-1997;
                                                                                                                                                                                                                                                              EP857973-A2.
                                                                                                                                                                                                                                                                                                 12-AUG-1998
                                    AAW64587;
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Gaps

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DB 2; Length 36; 0.47; nes 1; Indels

84.0%; Score 42; DB 2. 90.0%; Pred. No. 0.47; ive 0; Mismatches

Best Local Similarity 90.0 Matches 9, Conservative

Query Match

1 TRLTDKRGLK 10

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, liver, cirrhosis, hyperlipoproteinaemia, hyperlipidaemia,
hypercholesterolaemia, coronary heart disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 27; SEQ ID NO 30322; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                        Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID No 31152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG52504 standard; peptide; 343 AA.
                                                                                                                            26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-003468.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234539P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                  (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0180312P.
2000US-0207456P.
2000US-00603386.
2000US-0234687P.
2000US-0234687P.
2000US-0234687P.
                                                                        30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           169 TRLTRKRGLK 178
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                                                                                                                                                                                                                                                                                                        Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human liver peptide,
                                                                                                                                                                                                                                                                                                                                              WPI; 2001-483447/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 343 AA;
WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200157273-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-2000; 2
30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-FEB-2003
                                    09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG52504;
                                                                                                                                                                                                                                                                                                        Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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ABG52504
셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         applipation of applications are also as a major appropriation application of very-low density lipoproteins ((UDL), intermediate density lipoproteins ((UDL), intermediate density lipoproteins ((UDL), intermediate density lipoprotein (EDL), low density lipoproteins ((EDL) and lipoprotein a The present sequence can be used in the composition of the invention. The specification describes a composition that comprises LDL and applipatoreins for the binding and in vivo transport of nucleic acids. The composition is used to deliver nucleic acids to eukaryotic cells, in vivo or in vitro, for expressing a therapeutic polypeptide or antisense cancers (particularly non-small cell lung carcinoma), diabetes, cystic fibrosis and arteriosclerosis
                                                                                                                          Human apolipoprotein B-100; apoB-100; very-low density lipoprotein; VLDL; apolipoprotein; binding; in vivo transport; nucleic acid; binding domain; nuclear localisation sequence; gene therapy; cancer; cystic fibrosis; non-small cell lung carcinoma; diabetes; arteriosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition comprising nucleic acid bound to LDL or VLDL lipoprotein - used for delivering nucleic acid to cells for gene therapy and antisense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW96827-77 represent nucleic acid binding domains derived from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; foetal liver; gene expression; single exon nucleic acid probe.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84.0%; Score 42; DB 2; 90.0%; Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                        Nucleic acid binding domain from apoB-100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Moore JP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 16; Page 151; 293pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB37687 standard; peptide; 343 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (BAYU ) BAYLOR COLLEGE MEDICINE.
                                                                                                                                                                                                                                                                                                                                                                                  97US-00874807.
98US-00079030.
                                                                                                                                                                                                                                                                                                                                            98WO-US011927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hoogeveen RC,
                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-070331/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 51 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide #5193
                                                                                                                                                                                                                                                                                                                                              10-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                  13-JUN-1997;
14-MAY-1998;
                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                  WO9856938-A1
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                                                      22-APR-1999
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                                                                                                                                                                                                                                                                                                        17-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guevara JG,
                AAW96845;
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Matches
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Gaps

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(MOLE-) MOLECULAR DYNAMICS INC.

Chen W, Rank DR Hanzel DK, Penn SG,

WPI; 2001-488898/53

Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.

Claim 27; SEQ ID NO 31152; 658pp; English.

The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the probe further of complements of tragency in the probe hybridises at high etringancy to a nucleic acid molecule expressed in the human adult liver. If any be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. AEG47748-AEG5990 represent human liver single exon encoded peptides of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at the wipo.int/pub/published_pct_sequences

Sequence 343 AA;

Gape ô 84.0%; Score 42; DB 4; Length 343; 90.0%; Pred. No. 5.1; tive 0; Mismatches 1; Indels Query Match
Best Local Similarity 90.0*

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1 TRLTDKRGLK 10

169 TRLTRKRGLK 178 ò

Search completed: December 29, 2004, 12:28:50 Job time : 62.0227 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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December 29, 2004, 12:15:57; Search time 9.65909 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-8 50 Title: Perfect score: Sequence:

1 TRLTDKRGLK 10 Scoring table:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 200000000 Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	apolipoprotein B -	Д	apolipoprotein B-1	apolipoprotein B -	apolipoprotein B-1	probable periplasm	imidazoleglycerol-	sugar binding prot	multiple sugar-bin		pyruvate kinase (E	phosphotransferase	probable phosphotr	ganciclovir kinase	glutamine-fructose	btuR protein (impo	hypothetical prote	3	sodium/pantothenat	probable anthranil	hypothetical prote	hypothetical prote	heli	probable helicase	189.6K hypothetica	hypothetical prote	probable succinate	DHR38 protein - si	probable glycosylt
SUMMARIES	ΙD	532802	LPHUB	C60950	JH0102	E60950	A43654	D90206	AC2865	B97642	S17648	S17649	QQBEHS	T44214	T44029	B81246	T44695	T01873	H82022	F97787	T00782	F86359	T01955	H84486	4	ø	T48965	G81138	S58205	A10767
	88	7	Н	~	N	~	N	~	N	~	ч	N	-	~	N	N	N	N	~	~	N	N	N	N	N	~	N	0	~	7
	Query Match Length	965	4563	269	779	275	170	193	354	354	499	499	562	263	263	612	203	258	612	643	783	1029	1073	1241	1265	1678	1752	235	360	406
de	Query	84.0	84.0	76.0	76.0	72.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	70.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	8	9	9	0.99
	Score	42	42	38	38	36	35	35	35	35	35	32	35	35	32	32	34	34	34	34	34	34	34	34	34	34	34	33	33	33
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hypothetical prote	hypothetical prote	hypothetical prote	amsK protein - Erw	hypothetical prote	hypothetical prote	fimbrial assembly	apolipoprotein B -	RNA polymerase bet	RNA polymerase bet	DNA-directed RNA p	DNA-directed RNA p	DNA-directed RNA p	probable large Pro	hypothetical_prote	DNA topoisomerase
A90985	D85830	C64970	S52148	315296	T21384	F82546	865460	A86501	D72122	G81686	H71529	F81548	T35985	G87376	PN0152
~	N	~	N	~	~	N	~	0	~	7	N	7	N	~	7
406	406	406	407	411	487	490	1058	1252	1252	1252	1252	1262	1366	84	122
0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	0.99	64.0	64.0
	m	33	33	33	33	33	33	33	33	33	33	33	33	32	32
33	m														

ALIGNMENTS

RESULT 1

	S32802
	apolipoprotein B - crab-eating macaque (fragment)
_	C;Species: Macaca fascicularis (crab-eating macaque)
	C;Date: 06-Jan-1995 #sequence revision 06-Jan-1995 #text change 09-Jul-2004
	C;Accession: S32802
	R; Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchi
	Biochim. Biophys. Acta 1086, 326-334, 1991
_	A; Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional r
	A; Reference number: S32802; MUID: 92075708; PMID: 1742325
	A;Accession: S32802
	A;Status: preliminary
	A; Molecule type: mRNA
-	A;Residues: 1-596 <pap></pap>
	A; Cross-references: UNIPROT: Q28473; EMBL: X15737; NID: 938047; PIDN: CAA33755.1; PID: 99301
	C;Superfamily: apolipoprotein B
	Ouery Match 84.0%; Score 42; DB 2; Length 596;
	8; Pred. No. 1.8;
_	Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

226 TRLTRKRGLK 235 셤

1 TRLTDKRGLK 10

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upolipoprotein B-100 precursor - human
N;Contains: apolipoprotein B-26; apolipoprotein B-48; apolipoprotein B-74
C;Species: Be-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Date: 2B-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25679; A25267; A25266; A24320; A24684; A23817; A25774; A2
452; IG1909; IS39510; I39474; I39469; I84624; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sc.
DNA 6, 363-372, 1987
A;Title: DNA sequence of the human apolipoprotein B gene.
A;Title: DNA sequence of the human apolipoprotein B gene.
A;Accession: A27850
A;Molecule type: DNA
A;Residuae: 1-617, A', 619-1929, 'F', 1931-3318, 'D', 3320-3426, 'T', 3428-3431,'Q', 3433-3731,
A;Cross-references: UNIPROT:P04114; UNIPROT:P7842; UNIPROT:P78479; UNIPROT:O9UMNO; UNIR;Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A;Title: The complete sequence and structural analysis of human apolipoprotein B-100: r
A;Accession: A25679
A;Accession: A25679

A;Molecule type: mRNA A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA> A;Note: 1109-Agp was also found R;Knott, T.J.; Wallis, S.C.; Powell, L.M.; Pease, R.J.; Lusis, A.J.; Blackhart, B.; McC Nucleic Acids Res. 14, 7501-7503, 1986

Wed Dec

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A.Molecule type: mRNA
A.Residues: 4219-4337,'8',4339-4563 <PFI>
A.Cross-references: GBN36676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.;
Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Reference number: A24738; MUID:86042646; PMID:2932736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Molecule type: mRNA

A Keeldues: N', '3729-3731,'I', 3733-3875,'A', 3877-3948,'F', 3950-3963,'Y', 3965-3982,'S', 39

A Keeldues: N', '3729-3731,'I', 3733-3805,'B', '3745-1742.1; PID:9178736

B Krohen, S.H., Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai'

Science 238, 363-366, 1987

A Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in

A; Reference number: A40133; MUID:88018019; PMID:3659919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Mesiques: 51-75; 101-110; 129-139; 158-174; 197-207; 276-287; 298-304; 366-314; 526-532; 538-55 36; 1486-1498; 1537-1556; 1563-1572; 1601-1610; 1647-1661; 1697-1724; 1770-1781; 1859-1897; 1968-1498; 1537-1556; 1563-1572; 1601-1610; 1647-1661; 1697-1724; 1770-1781; 1859-1897; 1968-1498; 1537-1556; 1563-1572; 1601-1610; 1647-1661; 1697-1724; 1770-1781; 1859-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1898; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1898; 1970-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-1897; 1968-18
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A; Residues: 2169-2179 AHOS>
A; Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest on encodes the 250K apost 49, AA encoding 2180-Gln is substituted by the stop codon TAA, R; Yang, C.; Kim, T.W.; Weng, S.; Lee, B.; Yang, M.; Gotto Jr., A.M.
Proc. Natl. Acad. Sci. U.S.A. 87, 5523-5527, 1990
A; Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A; Reference number: A35783; MUID:90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Wolecule type: protein
A;Residues: 28-41;76-97,′I′,99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human apolipoprotein B 100-ape.
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A;Residues: 3056-3159 <MEH>
A;Residues: 3056-3159 <MEH>
A;Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
A;Cross-references: GB:X03045; NID:g28783; PIDN:CAA26850.1; PID:g929609
B;Hospattankar, A.V.; Higuchi, K.; Law, S.W.; Meglin, N.; Brewer Jr., H.B.
Biochem. Biophys. Res. Commun. 148, 279-285, 1997
A;Title: Identification of a novel in-frame translational stop codon in human intestine
A;Reference number: A29659; MUID:88049670; PMID:2445342
                                          R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E Atherosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than A;Feference number: A90084; MUID:86130855; PMID:3841481
A;Rocession: A29287
A;Rosidues: 3846-4298 <SHO>
R;Pfitzner, R.; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
Biol. Chem. Hoppe-Seyler 367, 1077-1083, 1986
A;Title: Isolation, expression and characterization of a human apolipoprotein B 100-8pp A;Reference number: A25572; MUID:87076044; PMID:3024665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NID:g178799; PIDN:AAA51754.1; PID:g178800 stop codon of the organ-specific mRNA for apo48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 2165-2179 <CH1>
A;Cross-references: GB:M18036;
A;Note: this mRNA includes the
A;Accession: A40133
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Ancession A2250
Ancession A225
                                                                                                                                                                                             A; Rocelle type: mRNA
A; Residues: 1-272,'N', 274-617,'A',619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; Residues: 1-272,'N',274-617,'A',619-1217,'E',1219-2091,'V',2093-2364,'T',2366-2679,'Q'
A; A; Croser serese: 68:X04506; NID:943331
R; Law, S.W.; Grant, S.W.; Higuchi, E,; Hogattankar, A.; Lackner, K.; Lee, N.; Brewer Jr
Proc. Natl. Acad. Sci. U.S.A. 83, 8142-8146, 1986
A; Title: Human liver apolipoprotein B-100 cDNA: complete nucleic acid and derived amino
A; Reference number: A94134; MUID:87041416; PMID:3464946
A; Accession: A2226
A; Molecule type: mRNA
A; Residues: 1-617,'A', 619-703,'P',705-792,'R',794-1270,'S',1272-1866,'G',1868-2036,'N', 2418-4220,'M',4222-4563 cLNA
A; Note: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
A; Note: the complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A9256; MUID:87008488; PMID:3759943
A; Accession: A2526
A; Molecule type: mRNA
A; Residues: 1-97,'I', 99-328,'V',330-644,'I',646-918,'P',920-3318,'D',3320-3426,'T',3428-A; Residues: 1-97,'I', 99-328,'V', 100-1000, A; Residues: 1-97,'I', 100-1000, A; Residues: 1-97,
                                                      human apolipoprotein B-100.
A)Reference number: A93639; MUID:87016385; PMID:3763409 A.Accession: A25263
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C;Species: Mesocricetus auratus (golden hamater)
C;Species: Mesocricetus auratus (golden hamater)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
C;Accession: JH0102
R;Smith, T.J.
submitted to GenBank, June 1990
A;Reference number: A38864
A;Accession: JH0102
A;Accession: JH0102
A;Residues: 1-779 <SMI>
A;Reference of the sequence from reference JH0101
R;Smith, T.J.; Hautamaa, D.; Maeda, N.
Gene 87, 309-310, 1990
A;Ritle: Sequence of the putative low-density lipoprotein receptor-binding regions of a.
A;Reference number: JH0101; MUID:90236327; PMID:2332175
A;Contents: annotation
A;Note: this sequence has been revised in reference A38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Kerwords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein F;435-445/Region: receptor binding F;646-656/Region: receptor binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polipoprotein B-100 - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B60950
R;Law, A.; Scott, J.
Lipida Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LD<sup>1</sup> A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
A;Accession: B60950
A;Residues: 1-275 <LAM.
A;Residues: 1-275 <LAM.
A;Cross-references: UNIPROT:Q7LZ77
C;Superfamily: apolipoprotein B
C;Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein
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R;Huang, M.L.W.; Cangelosi, G.A.; Halperin, W.; Nester, E.W.
Bacteriol. 172, 1814-1822, 1990
A;Title: A chronosomal Agrobacterium tumefaciens gene required for effective plant sign A;Reference number: A43654; MUID:90202696; PMID:2156804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable periplasmic receptor protein chvB precursor - Agrobacterium tumefaciens C;Species: Agrobacterium tumefaciens C;Species: 20-Feb-1993 #text_change 09-Jul-2004
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7
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Pred. No. 15;
1; Mismatches
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Pred. No. 15;
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                                                              (fragment)
                                                      apolipoprotein B - golden hamster
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80.0%;
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80.0%;
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A,Gene: apoB
C,Superfamily: apolipoprotein B
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Best Local Similarity 80..

Best Acal Similarity 80..
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Best Local Similarity 80.0
Matches 8; Conservative
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A; Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su FigleBoetle R. C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FBBS Lett. 170, 105-108, 1984
A; Title: Human apolipoprotein B partial amino acid sequence.
A; Reference number: A22006; WUID: 84208786; PMID: 637389
A; Accession: A22006
A; Accession: A22006
A; Accession: Detain
A; Residues: 873-892, K; 694-896 <LEI>
A; Residues: 313, L', 2115-3130, K; 3132-3133, P; 73135-3136, R' <LEZ>
A; Residues: 313, L', 2115-3130, R', 3132-3133, P; 73135-3136, R' <LEZ>
A; Residues: 313, L', 2115-3130, R', 1960 Protectin B gene.
A; Residues: 313, L', 2115-3130, R', 1960 Protectin B gene.
A; Reference number: A25564; MUID: 8705153; PMID: 2946672
A; Ride and Residues: amotectation; gene structure
B; Residues: amotectation; gene structure
C; R; Reference number: A30715; MUID: 87271140; PMID: 2866136
A; Contents: amotectaion; gene structure
C; R; Reference number: A30715; MUID: 87271140; PMID: 330480
A; Contents: amotectaion; gene structure
C; R; Reference number: A25605; MUID: 87201140; PMID: 330480
A; Contents: amotectaion; peparin binding and disulfide bond
C; R; Dashti, N.; Lee, D.M.; Mok, T.
B; Diabiti, N.; Lee, D.M.; Mok, T.
B; Diabitic Diabitic Contents: Bobles C. S. Bondjere, G.; Darnfore, C.; Wiklund, O.; Bjursell, G.; Bondjere, D.M.; Mok, T.
B; Diabition; Diabition; Diabition; Diabition; Diabition; Diabition; Diab
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Cipate: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
Cipate: 31, 3109-1120, 1990
A; Itipid Res. 31, 1109-1120, 1990
A; Itipid Res. 31, 1109-1120, 1990
A; Itipid Res. 31, 1109-1120, MUID: 90324804; PMID: 2373961
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C; Superfamily: apolipoprotein B
C; Superfamily: apolipoprotein C; Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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C;Species: Mesocricetus auratus (golden hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: C60950
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Best Local Similarity 80.0
Matches 8; Conservative
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216 SRLTRKRGLK 225
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Best Local Similarity
Matches 9; Conserv
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A;Status: preliminary

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multiple sugar-binding periplasmic receptor chve precursor [imported] - Agrobacterium to C. Species Agrobacterium tumefaciens
C. Species 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C. Accession: B97642
R. Scoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, S.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
R. Science 294, Salinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; R. Title, Senome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumes. A; Reference number: A97359; MUID:21608551; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1.354 <KUR>
A,Cross-references: UNIPROT: P25548; GB: AE007869; PIDN: AAK88091.1; PID:g15157521; GSPDB:C
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R;Allert, S.; Ernest, I.; Poliszczak, A.; Opperdoes, F.R.; Michels, P.A.M.
Eur. J. Biochem. 200, 19-27, 1991
A;Title: Molecular cloning and analysis of two tandemly linked genes for pyruvate kinasc
A;Reference number: S17648; MUID:91348039; PMID:1879424
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A;Molecule type: DNA
A;Residues: 1-499 <ALL.
A;Residues: U-499 <ALL.
A;Cross-treferences: UNIPROT: P30615; EMBL:X57950; NID:g10947; PIDN:CAA41018.1; PID:g10948|
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A Pathway: glycolysis
C; Superfamily: pyruvate kinase
C; Keywords: ATP biosynthesis; glycolysis; magnesium; metalloprotein; phosphotransferase;
F; 50, 212, 233/Binding site: substrate phosphate (Arg, Ser, Arg) #status predicted
F; 239/Active site: Lys #status predicted
F; 298, 333/Binding site: potassium (Gln, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Description: catalyzes the transphosphorylation of phosphoenolpyruvate and ADP to pyru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pyrivate kinase (EC 2.7.1.40) isoform 1 - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pyruvate kinase (EC 2.7.1.40) isoform 2 - Trypanosoma brucei
C;Species: Trypanosoma brucei
C;Species: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S17649
R;Allert, S.; Ernest, I.; Poliszczak, A.; Opperdoes, P.R.; Michels, P.A.M.
Bur. J. Blochem. 200, 19-27, 1991
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Pred. No. 41;
2; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70.0%; Score 35; DB 2;
70.0%; Pred. No. 30;
tive 1; Mismatches ;
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A, Map position: circular chromosome
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Best Local Similarity 70.0
Matches 7; Conservative
                                   141 TSITDKLGLK 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | :||| |||
141 TSITDKLGLK 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 RLTDKRGL 9
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A,Molecule type: DNA
A,Residues: 1-193 <KUR>
A,Cross-references: UNIPROT:033773; GB:AE006641; NID:913813761; PIDN:AAK40907.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GEOFFE E. W.

A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Aceference number: AB2577; MUD:21608550; PMID:11743193
A.Aceference number: AB2577; MUD:21608550; PMID:11743193
A.Status: preliminary
A.Status: preliminary
A.Residuss: 1-354 «KUR»
A.Residuss: 1-364 «KUR»
A.Residuss: 1-364 «KUR»
A.Residus: Coss-references: UNIPROT:P25548; GB:AE008688; PIDN:AAL43337.1; PID:g17740831; GSPDB:GCGenetics:
A.Gene: chvE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C,Genetics:
A,Gene: hisB
C,Superfamily: imidazoleglycerol-phosphate dehydratase; imidazoleglycerol-phosphate dehy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sugar binding protein (imported) - Agrobacterium tumefaciens (strain C58, Dupont)
CiSpecies: Agrobacterium tumefaciens
CiSpecies: Agrobacterium tumefaciens
CiAccession: Ac2865
CiAccession: AC2865
CiAccession: AC2865
CiAccession: AC2865
CiAccession: AC2865
CiAccession: AC2865
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CiAccession (CiAccession)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                inidazoleglycerol-phosphate dehydratase (hisB) [imported] - Sulfolobus solfataricus Gispecies: Sulfolobus solfataricus Gispecies: Sulfolobus solfataricus Gispecies: Sulfolobus solfataricus Cispecies: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 Gistocession: D90206 Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001 Gistocession: Sulfolobus solfataricus complete genome.

A;Reference number: A99139
A;Accession: D90206
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                                                                                                                                                                                         Length 170;
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                                                                                                                                                                                Score 35; DB
Pred. No. 15;
1; Mismatches
A;Molecule type: DNA
A;Residues: 1-170 <HUA>
A;Cross-references: UNIPROT:P25548; GB:M30318
                                                                                                                                                                       Query Match
Best Local Similarity 70.0%;
Matches 7; Conservative 1
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Best Local Similarity 70.0
Matches 7; Conservative
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81 TALGDKRGIK 90
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Gispecies: human herpesvirus 6 (strain HST)
Cispecies: human herpesvirus 6
A;Variety: strain HST
A;Variety: strain HST
Cipate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
Cispecies: Hand-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
Cispecasion: T44029
Cispecasion: T44029
A;Virol. 73, 8053-8063, 1999
A;Title: Comparison of the complete DNA sequences of human herpesvirus 6 variants A and A;Reference number: Z22732; MUD: 99412319; PMID: 10482554
A;Accession: T44029
A;Accession: T44029
A;Reference number: Z22732; MUD: 99412319; PMID: 10482554
A;Residues: 1-563 <ISBS
A;Residues: 1-564 <IRBS
A;Residues: 1-564 <IRBS
A;Residues: 1-564 <IRBS
A;Residues: 1-564 <IRBS
A;Res
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*Residues: 1-612 <TET-
A;Cross-references: UNIPROT:Q9KLP9; GB:AE002361; GB:AE002098; NID:g7225245; PIDN:AAF4050
A;Experimental source: serogroup B, strain MC58
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Kyeywords: aminotransferase; isomerase
F;2-612/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status pred:
F;2/Active site: Cys #status predicted
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Pred. No. 46;
2; Mismatches 1; Indels
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Pred. No. 50;
0; Mismatches 1; Indels
                                                                                 Length 563
                                                                                                                                                                       1; Indels
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C;Superfamily: human cytomegalovirus phosphotransferase
                                                                        Score 35; DB 2
Pred. No. 46;
2; Mismatches
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Similarity 66.7%;
6; Conservative ;
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Local Similarity 87.5%;
hes 7; Conservative (
                                                                                 70.0%;
                                                                                                                66.78;
                                                                                                                                                                  6; Conservative
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422 RMTDKRGCR 430
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                                                                            Query Match
Best Local Similarity
Matches 6; Conserv
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...... molecular cloning and analysis of two tandemly linked genes for pyruvate kinase A, Reference number: S17648; MUID:91348039; PMID:1879424
                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-499 <ALL.>
A; Residues: 1-499 <ALL.>
A; Residues: 1-499 <ALL.>
A; Residues: 1-499 <ALL.>
A; Cross=references: UNIPROT: P30616; EMBL: X57951; NID:g10949; PIDN: CAA41019.1; PID:g10956
A; Experimental source: strain 427
C; Function: actalyzes the transphosphorylation of phosphoenolpyruvate and ADP to pyru A; Pathway: glycolysis (C; Superfamily: pyruvate kinase (C; Superfamily: pyruvate kinase (C; Keywords: APP biosynthesis; glycolysis; magnesium; metalloprotein; phosphotransferase; E; 203, 212, 263/Binding site: substrate phosphate (Arg, Ser, Arg) #status predicted F; 239, Active site: Lys #status predicted F; 239, Mattive site: potassium (Gln, Glu) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       At yearlets: inumin interpolations of Attaches interpolations of Attaches inumin interpolations of Attaches interpolations of Att
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CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: human herpesvirus 6
CiSpecies: Juc-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
CiAccession: E36769
Bilawrence, G.L.; Chee, M.; Craxton, M.A.; Gompels, U.A.; Honess, R.W.; Barrell, B.G.
A; Virol. 64, 287-299, 1990
A; Title: Human herpesvirus 6 is closely related to human cytomegalovirus.
A; Reference number: A33560; MUID: 90080132; PMID: 2152817
A; Accession: E36709
A; Molecule type: DNA
A; Residues: 1-562 < LAM>A; Residues: 1-562 < LAM>CROSB-TEGERENCES: UNIPROT: P24446; GB: M68963; GB: M28243; NID: 9325494; PIDN: AAA65577.1; C; Superfamily: human cytomegalovirus phosphotransferase
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Matches 6; Conservative
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171 RLTDRRGI 178
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6; Conserva
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Search completed: December 29, 2004, 12:39:07 Job time : 11.6591 secs

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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNOV-1996 (TrEMBLrel. 24, Last annotation update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Apolipoprotein B (Fragment).
Apolipoprotein B (Fragment).
Bukacae fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota / Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Cararrhini; Cercopithecidae;
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BEDILNES-29707508; PubMed=1742325;
Pape M.E., Castle C.K., Murray R.W., Funk G.M., Hunt C.E.,

Marotti K.R., Melchior G.W.;
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les 9; Conservative
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NCBI_TaxID=9541;
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258 TRLTRKRGLK 267
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Q7nhs0 gloeobacter
Q7yqm8 hycrimene a
Q7yqm8 hycrimene a
Q7yqm4 rousettus a
Q7yr04 chaetophrac
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                                                                                                                   December 29, 2004, 12:13:11; Search time 58.4091 Seconds (without alignments) 98.508 Million cell updates/sec
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082788
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(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q28473
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033773 sulfolobus
Q885r4 bacteroides
Q72jp7 thermus the
Aa831069 thermus the
Q9Cqm3 m mus muscu
Q9Cqm3 m gmsculu
P25548 agrobacteri
Q7tn65 atherurus a
Q7tn65 trypanosoma
P30615 trypanosoma
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Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Aotinae, Aotus.
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MEDLINE-22761261; PubMed=12878460;
MEDLINE-22761261; PubMed=12878460;
Amrine-Madgen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 2225-240(2003).
EMBL; AFS48396; AAP97352.1; -.
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Last annotation update)
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Pred. No. 7.8;
0; Mismatches
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Q6L705
BAD18895
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Q8A5R4
Q72JP7
AAS81069
Q9CQM3
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CHVE_AGRT5
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KPY2_TRYBB
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90.0%;
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SEQUENCE FROM N.A.
                                    NCBI_TaxID=9606;
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P04114; 000502; Q13787;
01-N0V-1986 (Rel. 03, Created)
01-N0V-1986 (Rel. 03, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Apollboprotein B-100 precursor (Apo B-100) [Contains: Apolipoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carlsson P., Darnfors C., Olofsson S.O., Bjursell G.; "Analysis of the human apolipoprotein B gene; complete structure of
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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"Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional regulation.";
Biochim. Biophys. Acta 1086:326-334(1991).
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                                                                                                     SEQUENCE FROM N.A.
TISSUE-Liver;
Murray R.;
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
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Gene 49:29-51(1986).
BMB1, M15421, AA55758.1; -..
PIR, A27850, LPHUB.
GO, GO:0005576; C:extracellular; NAS.
GO; GO:0005319; F:lipid transporter activity; NAS.
GO; GO:0006869; P:lipid transport. NAS.
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Pred. No. 11;
0; Mismatches 1
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Pred. No. 68;
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MEDLINE=87191999; PubMed=2883086;
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90.0%;
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PIR; S32802; S32802.
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SEQUENCE OF 3109-4563 FROM N.A.
MEDLITES $5300528; Pubmed=2994225;
Knott T.J., Rall S.C. Jr., Innerarity T.L., Jacobson S.F., Urdea M.S.,
Levy-Wilson B., Powell L.M., Pease R.J., Eddy R., Nakai H., Byers M.,
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[10]
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MEDLINE=86041888; PubMed=3903660;
Mehrabian M., Schumaker V.N., Fareed G.C., West R., Johnson D.F.,
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MEDLINE=86093680; Pubmed=3841204;
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MEDLINE-87161758; PubMed-3030729;
Cladaras C., Hadzopoulou-Cladaras M., Nolte R.T., Atkinson D.,
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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MEDIINE=85270450; PubMed=3860836;
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VARIANT LEU-2739.
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MEDLINE=87039351; Pase R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
Knott T.C., Pease R.J., Powell L.M., Wallis S.C., Rall S.C. Jr.,
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VARIANTS FDB GLN-3527 AND CYS-3558.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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90.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97044521; PubMed=8889592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND ILE-3921.
MEDLINE-98141125; PubMed=9490296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mutat. 10:160-163(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 25, TrEMBLrel. 25, TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Apolipoprotein B (Including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 90.0
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01-OCT-2003
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Matches

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RESULT 6

OBLCXO

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OTRIO, 10-007-2003 (TERBLRel. 25, Created)
01-007-2003 (TERBLrel. 25, Last sequence update)
01-007-2003 (TERBLrel. 25, Last annotation update)
01-007-2003 (TERBLrel. 25, Last annotation update)
01-007-2003 (TERBLrel. 25, Last annotation update)
Diocros blocortein B (Fragment).
Diocros blocortein B (Black rhinoceros).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Eutheria, Perissodactyla, Rhinocerotidae, Diceros.
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430 AA
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                                                                                                                                                                                                                                                                                     76.0%;
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(TrEMBLrel. 26, I
(TrEMBLrel. 26, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G112465 protein.
OrderedLocusNames=g112465;
Gloeobacter violaceus.
                                                                                                                                                                                                                                                                                                            Local Similarity 80.0
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264 SRLTRKRGLK 273
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Les 7; Conserv
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SEQUENCE 430 AA
                                                                                                                                                                 Lipoprotein.
NON TER
NON TER 42
SEQUENCE 421
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01-MAR-2004
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4-0CT-2003 (TrEMBLrel. 25, Last annotation update)
4-0CT-2003 (TrEMBLrel. 25, Last annotation update)
6-0CT-2003 (TrEMBLrel. 25, Last annotate)
                                                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                       Length 4563;
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                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                  4563 AA; 515553 MW; 030B34167CEDC63C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY086357, AAM64425.1; -.
Hypothetical protein.
SEQUENCE 132 AA; 14674 MW; A3698270AE88CD31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein.
     GO; GO:0005319; F:lipid transporter activity; IEA. GO; GO:000659; P:lipid transport; IEA. Interbro; IPR009454; DUF1081. Interbro; IPR001947; Lipid transprt_N. Pfam; PF06448; DUF1081; 1. Pfam; PF01347; Vitellogenin_N; 1.
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                                                                                                                                                                                                                                                    Score 42; DB 2
Pred. No. 97;
0; Mismatches
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                                                                                                                                                                                                                                                  84.0%;
90.0%;
                                                                                                                                                                                                                                                                                                  9; Conservative
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                                                                                                                                                                                                                                                                        Local Similarity
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[1]
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                                                                                                                                                                           Lipoprotein.
SEQUENCE 4
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STRAIN=PCC 7421,

XX MEDLINE=22977440; PubMed=14621292;

RA Maraura Y., Kanacho T., Sato S., Minuro M., Miyashita H., Tsuchiya T.,

RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,

RA Takeuchi C., Yamada M., Tabata S.;

RA Takeuchi C., Yamada M., Tabata S.;

RY "Complete genome structure of Gloeobacter violaceus PCC 7421, a

RY "Complete genome structure of Gloeobacter violaceus PCC 7421, a

RY "Complete genome structure of Gloeobacter violaceus PCC 7421, a

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SEQUENCE FROM N.A.

MEDLINE-22761261, bubwed=12878460,

Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.,

"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.",

Mol. Phylogenet. Evol. 28:225-240(2003).
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Pred. No. 52;
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421 AA; 46747 MW; D47B77BD4F864FD1 CRC64;
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NCBI_TaxID=33072;
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Last annotation update)
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Q7TN68

RESULT 7

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O7TN68

Query Match

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RESULT 10

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Gaps
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Rousettus amplexicaudatus (Common rousette).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;

Pteropodinae; Rousettus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE-2761261.

Amrine-Madean H., Koepfli K.-P., Wayne R.K., Springer M.S.;

Amrine-Madean H., Koepfli K.-P., Wayne R.K., Springer M.S.;

"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for ethherian relationships.";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243383; AAPS0771.1;
MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling
evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL; AFS48436; AAP97392.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22761261; PubMed=12878460; Mayne R.K., Springer M.S.; Amrine-Madsen H., Koepfil K.-P., Wayne R.K., Springer M.S.; "A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
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Chaetophractus villoaus (South American armadillo).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Edentata; Dasypodidae; Chaetophractus.
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438 438
438 AA; 48734 MW; 2BDB5BCBF4E2CC41 CRC64;
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438 438
438 AA; 48597 MW; 41C890DEAF95C872 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
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Pred. No. 54;
1; Mismatches
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43
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                         MEDLINE=22761261; PubMed=12878460;
Amrine-Madeen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolitoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AY243375; AAP50763.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
"A new phylogenetic marker, apolipoprotein B, provides compelling evidence for eutherian relationships.";
Mol. Phylogenet. Evol. 28:225-240(2003).
EMBL, AF548435; AAP97391.1; -.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Chiroptera; Megachiroptera; Pteropodidae;

Pteropodinae; Nyctimene.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Chiroptera, Megachiroptera, Pteropodidae,
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432 432
432 AA; 48171 MW; F27B7AB39604732C CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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01-0cT-2003 (TrEMBLrel. 25, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
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80.0%; Pred. No. 54;
tive 1; Mismatches
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Matches 8; Conservative
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275 SRLTRKRGLK 284
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436
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SEQUENCE FROM N.A.
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Search completed: December 29, 2004, 12:37:36
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MEDLINE=22761261; PubMed=12878460;
Amrine-Madsen H., Koepfli K.-P., Wayne R.K., Springer M.S.;
An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships ";
Mol. Phylogenet. Evol. 28:225-240(2003).
                                                                                                                                                                                                                                                                                                                                                   Agouti paca (Paca).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Hystricognathi, Agoutidae, Agouti.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2004 (TrEMBLrel. 26, Last annotation update)
Apolipoprotein B (Fragment)
Hydrochoerus hydrochaeris (Capybara) (Carpincho).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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MEDLINE=22761261; PubWed=12878460;

Amrine-Madgen H., Kooplin K.-P., Wayne R.K., Springer M.S.;

An new phylogenetic marker, apolipoprotein B, provides compelling evidence for eucherian relationships ";

Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL; AY243369; AAP507571; --

InterPro; IPR000871; Beta_lactamase_A.
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                                                                                                Query Match 76.0%; Score 38; DB 2; Length 445; Best Local Similarity 80.0%; Pred. No. 55; Matches 8; Conservative 1; Mismatches 1; Indels
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                                                         445 445 445 445 AW; 2DA5DC3ED2F0FDD2 CRC64;
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445 AA; 49721 MW; 34AF7ABE90F121EF CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Apolipoprotein B 100 (Fragment).
                                                                                                                                                                                                                                                          445 AA
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Mol. Phylogenet. Evol. 28:225-240(2003).

EMBL, AY243378; AAP50766.1; -.

Lipoprotein. 1 1 1

NON TER 445 445

SEQÜENCE 445 AA3, 49564 MW; 2DA5DC3ED2
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288 SRLTRKRGLK 297
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445 445
445 AA; 49520 MW; CBBA2DD53D7A18D2 CRC64;
PROSITE; PS00146; BETA_LACTAMASE_A; UNKNOWN_1.
Lipoprotein.
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RESULT 1
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                                                                                                                December 29, 2004, 12:10:41; Search time 54.9205 Seconds (without alignments) 58.786 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Aay30694 Apo-B100
Aay30695 Apo-B100
Abx43240 Human PuN
Abg97506 Human PuN
Abc98868 Human gen
Adx71826 Human sec
Ade38441 Human pro
Ady38449 Human sec
Ads38441 Human pro
Ady30684 Apo-B100
Aay30688 Apo-B100
Aay30688 Apo-B100
Aay30688 Apo-B100
Aay30687 Apo-B100 Human gen Human kin Human sec Human pro Marker ge Marker ge Apo-B100 Aae14541 Human apo Aaw96876 Nucleic a Heparin b ADP29449 ADE38441 ADJ75552 AAY30684 AAY30683 AAY30683 AAY30682 AAY30685 AAY30687 AAY30696 ABR43240 ABG97506 ABO58868 AAW57209 AAE14541 AAW96876 AAW57205 ADK71826 AAW41261 H В Query Match Length Result No.

Aaw64587 Human apo Aaw96845 Nucleic a Abb37687 Peptide # Abg22504 Human liv Aar72704 Human apo Aar34031 Sequence Adj57400 Human apo Aay31237 Human Apo Aay31237 Human Apo Aay1262 Apolipopr Aaw96826 Amino aci Aau98981 Human apo Add48677 Human apo Add48678 Human apo	Human Human
AAW64587 AAN96845 AAB37687 AAB37687 AAB52504 AAR72704 AAR72704 AAV31237 AAW41262 AAW98981 AAD48677 AAR40253 ABC79140 ADF43408 ADF43408 ADF43418871	AD033445 AD033447
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76.11	76.1
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ALIGNMENTS

AAY30694 standard; peptide; 9 AA

AAY30694;

AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgent non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis. Apo-B100; proteoglycan receptor mutation, atherosclerosis, low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion. Apo-B100 derived peptide showing a proteoglycan receptor mutation. Claim 17; Page 57; 70pp; English. 99WO-US004805 98US-0077618P Innerarity TL, Boren JOS; (first entry) (REGC) UNIV CALIFORNIA. WPI; 1999-551509/46. Homo sapiens. WO9946598-A1 05-MAR-1999; 10-MAR-1998; 17-NOV-1999 16-SEP-1999 Synthetic.

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atherosclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent enterosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used as an in vivo model system for the study of atherosclerosis. Thus the assays may be used to dentify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                            Score 41; DB 2; Length 9;
Pred. No. 1.7e+06;
L; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                            AAY30696 standard; peptide; 9 AA.
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                                                         93.2%;
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                      Conservative
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                                                         Query Match
Best Local Similarity
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        Sequence 9 AA;
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also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                                                                                                                                                                                                                                                        100.0%; Score 44, DB 2; L
llarity 100.0%; Pred. No. 1.7e+06;
Conservative 0; Mismatches 0;
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Best Local Similarity
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(CURA-) CURAGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HTV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC5955 to ACC59989 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated profession of the ABR43270 and antial to PMM-1. It of PMM-1 and the ABR43270 and antial experiment, nootropic, neuroprotective, carebroprotective, antial expectation, antinflammatory and thyromimetic activities, and can be used in gene therapy. The PMMM polypeptides and polymucleotides are useful in diagnosing, treating and preventing diseases or conditions associated with the decreased expression or overaxpression of PMMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AlDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                             protein modification and maintenance molecule; PMMM; cytostatic;
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Yang J, Lu DAM;
SY, Ramkumar J, Be
AE, Hafalia AJA, 1
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Gietzen KJ, Yang
Bson TW, Lee SY, F
In UK, Kable AE, F
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i JX, Griffin JA, Gietzem
Duggan BM, Richardson TW,
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                                                                                                                                                                              ABR43240 standard; protein; 404 AA
                                                                                                                                                                                                                                                                                                                                                                    Human PMMM-1 protein SEQ ID NO:1.
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2001US-032433P.
2001US-034333P.
2001US-0346198P.
2001US-0348897P.
2001US-0332423P.
2001US-0334455P.
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2002US-0351928P,
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Li JX, Gr
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TRLTRKGLK 9
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N-PSDB; ACC59959.
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09-NOV-2001; 2
16-NOV-2001; 2
28-NOV-2001; 2
28-NOV-2001; 2
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26-OCT-2001;
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Marquis JP,
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sequences of PMMM. The PMMMS or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polymucleotide and compounds that specifically bind to or modulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein interactions, drug-target interactions, and gene expression profiles
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Pred. No. 1.1e+02;
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2001US-0277239P.
2001US-0277327P.
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2001US-0277791P.
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2001US-0279036P.
2001US-0279344P.
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2001US-0275579P.
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2001US-0338375P.
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                                                                                                                                                                                                                                                                          6; Conservative
                                                                                                                                                                                                                                                                                                                                                     367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human NOVX25 protein.
                                                                                                                                                                                                                                                                                                                         1 TRLTRRGLK 9
                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                         Sequence 404 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200272770-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2001;
14-MAR-2001;
20-MAR-2001;
20-MAR-2001;
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27-MAR-2001;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2001;
21-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001;
02-APR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-MAR-2001;
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polypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, preferably a NOVX-associated disorder. The NOVX nucleic acids, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as cancers, Hodgkin disease, Von Hippel-Lindau Syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, troke, tuberous sclerosis, ataxia- palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxia- palsy, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, depression, pain, cobesity, Crohn's disease, addiction, anxiety, depression, pain, cobesity, Crohn's disease, atterporosis, inflammatory bowel disease, infertility, inflammatory bowel disease, atherosclerosis, hypertension, scleroderma, hemophilia, diabetes, pancreatitis, autoimmune disease, asthma, arthritis, immunodeficiencies, HVV, viral, bacterial or parasitic infections, or graft-versus-host disease. The nucleic acids and palypeptides may also be used as targets for the identification of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                           New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecules that modulate or inhibit e.g. neurogenesis, cell defferentiation, cell proliferation, haematopoiesis, wound healing and anglogenesis, in gene therapy, in generation of antibodies that bind immunospecifically to NOVX substances for use in therapeutic or infagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present amino acid sequence represents a human NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                    , Malyankar UM, Gerlach VL;
Gusev VY, Kekuda R, Pena CEA;
                                                                                                                                                                                                                                                                                                   The present invention relates to a new polypeptide (NOVX). The NOVX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.5%; Score 35; DB 5; Length 548; 66.7%; Pred. No. 1.5e+02; ive 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human genome derived single exon protein #5102.
                Tchernev VT,
    Vernet CA, TCDermousen BD, Patturajan M, Taupier RJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABO58868 standard; protein; 151 AA.
                                                                                                                                                                                                                                                                Claim 1; Page 161; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03-APR-2002; 2002US-00029386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-2002; 2002US-00029386,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention
                               Zerhusen BD, Par
7, Gangolli EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||:|:|||:
515 TRITKRGLE 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TRLTRRGLK 9
                                                                                                                                                                                                                        Parkinson's disease.
                                                                                                  2002-713508/77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                     N-PSDB; ABS78750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 548 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003194704-A1.
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                  Spytek KA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2003.
                                                      Zhong M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABO58868;
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                                                                                                  WPI;
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or iragments, and sequences in the specification, or their complements or iragments, and sequences in the specification. The probe is a single exon probe that thybridises under high stringency conditions to a nucleic acid molecule exclusive faint of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially-care addressable set of single exon nucleic acid probes for measuring human pene expression (comprising a plurality of single exon microarray for measuring human gene expression, a method of madernay for measuring human gene expression, a method of contiguous amino acids of any of the abover mentioned amino acid contiguous amino acids of any of the abover mentioned amino acid solution and/or licensing single exon probes or microarray to soluted antibody that binds specifically to a peptide cited above, a soluted antibody that binds specifically to a peptide cited above, solutions and/or licensing single exon probes or microarray to a customer destring to measure gene expression, a method of providing seconds of selling and/or licensing single exon probes or microarrays to a customer destring to measure gene expression and acids and paraly in a method of providing to a customer destring to measure gene expression of a single exon probe crock a customer destring to measure gene expression of a single exon probe crock including data on the expression of a single exon probe crock and addition, the probes may be used as tools for surveying crossesion analysis. The probes may be used as tools for surveying crossesion analysis. The probes may be used as tools for surveying crossesion analysis. The probes may be used as tools for surveying alternative splicing events, in detecting and characterising alternative splicing exon probe protein of the invention. Note: The sequence data for forma
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                                                                                                                                                                                        New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human kinase and phosphatase KPP-3 protein.
                                                                                                                                                                                                                                                                                                    Claim 45; SEQ ID NO 32502; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADK71826 standard; protein; 311 AA.
                                                                                                            Hanzel DK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAY-2004 (first entry)
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Aatches 7; Conservative
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                                                                                                                                                    WPI; 2004-119264/12
                  (RANK/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                         Rank DR,
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                                                                                                                                                                                                                                                            surveying tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 151 AA;
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                                                                                                         Penn SG,
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RESULT 8 ADP29449

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The invention relates to a novel isolated polypeptide which is a human kinase and phosphatase (KPP). The polypeptide of the invention demonstrates cardiovascular, antiantication cotto. Wypotensiave, vasotropic, antianianiania, anti-HIV, antiallergic, antianflammatory, antianginal, anti-HIV, antiallergic, antiathmatic, immunosuppressive, antithyroid, dermatological, antiallergic, antighate, nephrotropic, antigout, gastrointestinal, neuroprotective, catepathic, antiarthritic, uropathic, ophthalmological, antitheumatic, antiparkinsonian, nootropic, antilipaemic, antiparasitic, antihelmunic, antibacterial, virucide, protozoacide and funglicide activities. The kinase and phosphatase (KPP) polyuncleotides, polypeptides, agonists and antipacterial wirucide, protozoacides, polypeptides, agonists and antagonists may be useful for diagnosing, treating or preventing antagonists may be useful for diagnosing, treating or preventing cardiovascular diseases, immune system disorders and viral, bacterial, fungal, parasitic, proliferative disorders and viral, bacterial, fungal, parasitic, protozoan or helminthic infections. Purthermore, the molecules of the invention may be useful for creating transgenic animals to model human disease and during gene therapy. The current sequence is that of a human KPP protein of the invention.
human; kinase; phosphatase; KPP; cardiovascular; antiarteriosclerotic; hypotensive; vasotropic; antinflammatory; antianginal; anti-HIV; dermialergic; antiasthmatic; immunosuppressive; antithyroid; dermatchogical; antidabetic; nephrotropic; antidout; gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic; ophthalmological; antithematic; antiparkinsonian; nootropic; antiparamit hepatotropic; antiboriatic; haemostatic; cytostatic; antilpaemic; antiparasitic; cytostatic; antilpaemic; antiparasitic; cardiovascular disease; immune system; neurological; growth; development; call proliferation; viral; bacterial; fungal; parasitic; protozoan; single nucleotide polymorphism; SNP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tran UK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human kinases and phosphatases, useful for diagnosing, treating or preventing atherosclerosis, hypertension, AIDS, allergy, multiple sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Richardson TW, Marquis JP, Swarnakar A, Tang YT;
Emerling BM, Jin P, Wilson AD, Yue H, Gietzen KJ;
Yang YG, Lee SY, Khare R, Elliott VS, Hafalia AJA;
,, Ramkumar J, Gururajan R, Tribouley CM, Chien D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 3; 347pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2002; 2002US-0413910P.
27-SEP-2002; 2002US-0414296P.
11-OCT-2002; 2002US-0417821P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-AUG-2002; 2002US-0406172P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-AUG-2003; 2003WO-US026635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baughn MR, Richardson TW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becha SD, Emerling BM,
Chang H, Yang YG, Lee G
Chawla NK, Ramkumar J,
Murage J;
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N-PSDB; ADK71885.
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                                                                                                                                                                                                                                                                                                                                                        WO2004018641-A2.
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                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
ADP29449 standard, protein, 933 AA.
                                                                                                                    Human secreted protein SEQ ID #216
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2002US-0411048P.
2002US-0411052P.
2002US-0411075P.
2002US-0411073P.
2002US-041101P.
2002US-0411111P.
                                                                                                                                                                                                                                                                                                                                              28-AUG-2003; 2003WO-US026780
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02-MAY-2003; 2003US-0467203P
02-MAY-2003; 2003US-0467230P
                                                                            (first entry)
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                                                                                                                                                                                                                        Homo sapiens.
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17-SEP-2002;
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                                                                            12-AUG-2004
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                                    ADP29449;
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Gaps

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Length 311;

77.3%; Score 34; DB 8; Length 311 100.0%; Pred. No. 1.3e+02; ive 0; Mismatches 0; Indels

Local Similarity 100.

Query Match Best Local S: Matches 7,

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This invention relates to a novel method of treating a human subject having a tumourigenic disorder or angiogenic disorder, caused by aberrant gene expression or activity of an isolated protein, by administering a modulator. The modulator may have cytostatic, antithyroid, antidiabetic or ophthalmological activity. The method is useful for treating a busing a tumourigenic or angiogenic disorder, in particular for treating cancer (for example breast cancer, colon cancer, lung cancer or prostatic cancer) and, for example Grave's disease and diabetic retinopathy. The present sequence is the amino acid sequence of the novel isolated human protein 1420 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating subject having tumorigenic disorder or angiogenic disorder caused by aberrant polypeptide e.g., N-formylpeptide receptor or nucleic acid, by administering a modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bronchial asthma; chronic obstructive pulmonary disease;
respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
gene therapy; marker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lightcap ES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marker gene related amino acid gequence SEQ ID NO:804.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lescon A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 102; 454pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hunter JJ, Macbeth KJ, Tsai F, Williamson MW, Rudolph-Owen LA;
                                                                                                                                                                                                                                                                                                                  13-AUG-2002; 2002US-0403046P.
22-AUG-2002; 2002US-0405155P.
27-AUG-2002; 2002US-040636IP.
12-NOV-2002; 2002US-0421195P.
12-NOV-2002; 2002US-04256P.
                                                                            2002US-0364517P.
2002US-0371075P.
2002US-0371507P.
                                                                                                               10-APR-2002; 2002US-0371507P.
16-APR-2002; 2002US-0372984P.
14-APR-2002; 2002US-0374194P.
24-MAY-2002; 2002US-0382955P.
                                                                                                                                                                                                31-MAY-2002; 2002US-0385023P.
14-JUN-2002; 2002US-0388853P.
17-JUN-2002; 2002US-0389395P.
                                                                                                                                                                                                                                                         25-JUN-2002; 2002US-0391324P.
15-JUL-2002; 2002US-0395944P.
22-JUL-2002; 2002US-0397726P.
                30-JAN-2003; 2003WO-US002588
                                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-2002; 2002US-0425456P
19-NOV-2002; 2002US-0427626P
10-DEC-2002; 2002US-0432122P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-) MILLENNIUM PHARM INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2003-646176/61.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid molecule for diagnosing, preventing or treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tumourigenic disorder, angiogenic disorder, aberrant gene expression, aberrant protein activity, cytostatic, antithyroid, antidiabetic, ophthalmological, cancer, breast cancer, colon cancer, lung cancer, prostatic cancer, Grave's disease, diabetic retinopathy, protein 1420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cytostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWES and is not in the specification.
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hakota S, Haishan L, Linnemann T;
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                                                                                                                                                                                                                                                                                                                                                                                                               Chu K, Lee E, Heatir K, Beaur, Huang MM, Kothakota S, Haisha ang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 1447; 428pp; English.
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                                                                                                                                                                                                                                                                                                                                                                         (FIVE-) FIVE PRIME THERAPEUTICS INC.
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    19-MAY-2003, 2003US-0471336P.
22-MAY-2003, 2003US-0472420P.
22-MAY-2003, 2003US-0472430P.
09-JUN-2003, 2003US-0476641P.
09-JUN-2003, 2003US-0485213P.
08-JUL-2003, 2003US-0485224P.
08-JUL-2003, 2003US-0485224P.
08-JUL-2003, 2003US-0485224P.
14-JUL-2003, 2003US-0485325P.
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                                                                                                                                                                                                                                                                                             2003US-0493370P
2003US-0493573P
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175 RLTRRGL 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                          14-JUL-2003; 15-JUL-2003; 15-JUL-2003;
                                                                                                                                                                                                                                                                                             08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Halenbeck RF
                                                                                                                                                                                                                                                                          08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                 Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADE38441;
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03-MAR-2004.

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which andulate atherosaclerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (FG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in alterosclerosis. The assays may be used to determine whether a therosclerosis and be used to determine whether
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a particular food or drug composition fends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in a animal or mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                 ypo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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                           Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0077618P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Innerarity TL, Boren JOS;
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                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                             WO9946598-A1
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                                                                                                                                                                                                                                                                                                                   16-SEP-1999
                                                                                                                                                                        Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present introductive pulmonary disease. The method comprises determining the expression level of a marker gene in a biological sample from a subject, comparing the expression level determined with the expression level of the marker gene in a biological sample from a healthy comprises and judging whether the subject has bronchial asthma or chronic obstructive pulmonary disease. The marker gene comprises: (a) a group of genes (S1) whose expression levels increase when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13; or (b) a group of genes (S2) whose expression levels decrease when respiratory epithelial cells are stimulated with interleukin-13. Also described: (1) a reagent (1) for centing for bronchial asthma or chronic obstructive pulmonary disease; (2) a kit for screening for a candidate compound for a therapeutic agent or treat bronchial asthma or chronic obstructive pulmonary disease; (4) an inducer that induces bronchial asthma or chronic obstructive pulmonary disease, (6) a therapeutic agent for producing an animal model for bronchial asthma or chronic obstructive pulmonary disease, (6) a therapeutic agent for pronchial asthma or chronic obstructive pulmonary disease, (6) a therapeutic agent for compound, a sthma or chronic obstructive pulmonary disease, comprising the compound cexpression of the gene through an RNA ieffect or an antibody recognising the marker gene, a riboryme, a polynucleotide that suppresses the expression of the gene through an RNA ieffect or an antibody recognising a protein encoded by a marker gene; and (7) a DNA chip for testing for a stronic obstructive pulmonary disease, on which and antiasthmatic activities, and can be used in gene therapy. The method componed is useful for testing for or excreening for a broader or an antibody and antiasthmatic activities, made and an expression of the gene productive pulmonary disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Testing for bronchial asthma or chronic obstructive pulmonary disease by comparing the expression level of a marker gene in a biological sample from a subject with the expression level of the gene in a sample from a healthy subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a method of testing for bronchial asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present
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sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                     Yamaya M, Kubo H, Nagai H, Izuhara K;
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                                                                                                                                                                                                 04-AUG-2003; 2003EP-00254857.
                                                                                                                                                                                                                                                       06-AUG-2002; 2002JP-00229312
20-MAR-2003; 2003JP-00077212
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Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                           (GENO-) GENOX RES INC
                                                                                                                                                                                                                                                                                                                                                                                                  Ohtani N, Sugita Y,
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                           Homo sapiens.
                                                                                 EP1394274-A2.
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AAY30684;

RESULT 1

Query Match

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Homo sapiens

98US-0077618P.

10-MAR-1998;

(REGC) UNIV CALIFORNIA

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Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                              AAY30686 standard, peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                               99WO-US004805
                                                     Innerarity TL, Boren JOS;
                                                                                                                                                                                                                                                                 17-NOV-1999 (first entry)
                                            (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                       9; Conservative
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                                                             WPI; 1999-551509/46.
                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                       Sequence 10 AA;
        WO9946598-A1
                          05-MAR-1999;
                                   10-MAR-1998;
                 16-SEP-1999.
                                                                                                                                                                                                                                                                                               Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                              05-MAR-1999;
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which condulate atheroselerosels. The peptides are derived from amino acids 3358 to 3367 of apo8100. The method comportses detecting compounds which affect clow density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding Such compounds can be used to reduce or prevent the formation of atheroselerotic lesions and prevent atheroselerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulates atheroselerosis and/or LDL-PG binding. They can compounds which modulates thereofererosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in atheroselerotic regions. Thus the assays may be used to determine whether compounds witch an apposition tends to stimulate or inhibit the formation of atheroselerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
                                                                                                                                                                                                         Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apo-B100; proteoglycan receptor mutation, atherosclerosis;
low density lipoprotein; proteoglycan; LDL, atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 5.4; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY30682 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                       Claim 17; Page 57; 70pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 90.00,
Local 9, Conservative
                                                                                                                  Boren JOS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                           atherosclerosis,
                                                                                                             Innerarity TL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                         Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
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98US-0077618P.

10-MAR-1998;

Innerarity TL, Boren JOS;

(REGC) UNIV CALIFORNIA.

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which andulate atherosaclerosis. The peptides are derived from anino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (FG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and mammals which express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in also be used to determine whether can particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polymoleotides can also be the and an animal or shown and an animal or reducing the severity of shown and an animal or reducing the severity of
                                    ifying compounds which affect binding of low density lipoprotein proteoglycan, used for, e.g. obtaining compounds for reducing
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low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion
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                                                                                                         Claim 17; Page 57; 70pp; English.
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Best Local Similarity 90.00
Pest Local 9; Conservative
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WPI; 1999-551509/46.
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                                Identifying
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Claim 17; Page 57; 70pp; English.

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receptor mutations. They were created to identify compounds which computed attentions. They peptides are derived from amino acids 3358 computate attenceslerosis. The peptides are derived from amino acids 3358 computed at a possible. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (EG). The method can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent atherosclerosis. The transgenic non-human animals and manmals which atherosclerosis, and in vivo assay methods for identifying compounds which medulate atherosclerosis and/or LDL-PG binding. They can set be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the confined and an animal or mammal reducing the severity of atherosclerosis in an animal or mammal
                       AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan
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Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 8.69118 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-13 Perfect score:

1 TRLTRRGLK 9 Scoring table: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	protein-tyrosine k	conserved hypothet	apolipoprotein B -	apolipoprotein B-1	probable ISRm25b t	hypothetical prote			glycerol dehydroge	-H		hypothetical prote	cal	\rightarrow	hypothetical prote	hypothetical 38.5K	6-phosphofructokin	hypothetical prote	hypothetical prote	protein B0205.5 [i	conserved hypothet	anaerobic ribonucl	hypothetical 21K p		hypothetical 20K p	myc protein - huma		ų	hypothetical prote
SUMMARIES	ID	A34076	AE1065	S32802	LPHUB	B95329	D72044	A86581	AI1291	AG1663	A84155	F95869	F87592	T05005	T07863	T35260	JC1175	S54978	T29926	G81430	A87912	F87342	E82452	JU0451	159116	A29867	179500	S77172	G87325	876916
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de	Query Match	77.3	77.3	76.1	76.1	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	75.0	72.7	72.7	72.7	72.7	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5
	Score	34	34	33.5	m,	33	33	33	33	33	33	33	33	33	33	32	32	32	32	31	31	31		31	31		31		31	31
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AE1065 conserved hypothetical protein STY4851 [imported] - Salmonella enterica subsp. enterica C,Species: Salmonella enterica subsp. enterica serovar Typhi A,Note: this species has also been called Salmonella typhi

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Gaps

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77.3%; Score 34; DB 1; Length 984; 100.0%; Pred. No. 90; ive 0; Mismatches 0; Indels

Local Similarity 100. les 7; Conservative

Query Match Best Local Matches 175 RLTRRGL 181

요 8

RESULT 2

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2 RLTRRGL

hypothetical prote probable acyl-coen	D-amino-acid oxida D-amino-acid oxida		₽ ⊶	hypothetical prote probable cobyrinic	ABC transporter pr probable phosphogl	beta-fructofuranos ribonucleoprotein	malate dehydrogena
A65020 B90399	JH0185 OXPGDA	JX0132 S43067	C87455 H75444	AD2219 T03545	T17948 T41375	S62332 C75418	A13372
0.0		1 1 2	0,0	0 0	0 0	0 0	7
279	345	347	364 393	393 435	462 466	466 531	774
70.5	70.5	70.5	70.5	70.5	70.5	70.5	70.5
31	333	311	31	31	31	31	31
30	288	 	37	39 40	41 42	4 4 6 4	45

ALIGNMENTS

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A.Wolecule type: mRNA
A.Residues: 1-984 cAIR.
A.Residues: 1-984 cAIR.
A.Cross-references: UNIPROT: P21709, GB:M18391, NID:G339716, PIDN:AAA36747.1; PID:G33971
A;Note: the sequence in GenBank entry HUWTKR, release 111.0, has the codons GCG for 398
R;Tuzi, N.L.
Submitted to the EMBL Data Library, November 1993
A;Description: An EGFR/eph chimeric receptor possesses ligand stimulated tyrosine kinas:
A;Reference number: S44280
A;Residues: 284280
A;Molecule type: mRNA
A;Residues: 286-397, A',399-580, QRDRAIDVDREDKLWLKPYVDLQAYEDPAQGALDF',583,625-984 <TUZ>
A;Cross-references: EMBL: Z27409; NID:g482916; PIDN:CAA81796.1; PID:g482917
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A/Cross-references: GDB:119875, OMIN:179610
A/Cross-references: GDB:119875, OMIN:179610
A/Cross-references: GDB:119875, OMIN:179610
C/Map position: 7432-7436
C/Map position: 74374
C/Map position: 74374
C/Map position: 74374
C/Map product: protein-tyrosine kinase receptor type eph; #status predicted <MAT>
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                                                                                                                        protein-tyrosine kinase (EC 2.7.1.112) receptor type eph 1 precursor - human N.Alternate names: receptor tyrosine kinase eph C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Accession: A34076; S44280 R; Hirai, H.; Maru, Y.; Hagiwara, K.; Nishida, J.; Takaku, F. Science 238, 1717-1720, 1987 A; Title: A novel putative tyrosine kinase receptor encoded by the eph gene. A; Reference number: A34076; MUID:88070650; PMID:2825356
RESULT 1
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A; Molecule type: mRNA
A; Residues: 1.617, 'A', 619-703,'P',705-792,'R',794-1270,'S',1272-1866,'G',1868-2036,'N',2)
A; Residues: 1.617, 'A', 619-703, 'L', 705-792,'R', 794-1270,'S',1272-1866,'G',1868-2036,'N',2)
A; Molec: the codons given for residues 704, 793, 1271, 2037, 2933, 3286, 3782, 4188, and
R; Chen, S.H.; Yang, C.Y.; Chen, P.F.; Setzer, D.; Tanimura, M.; Li, W.H.; Gotto Jr., A.M.
A; Dill. Chem. 261, 12918-12921, 1986
A; Title: The complete cDNA and amino acid sequence of human apolipoprotein B-100.
A; Reference number: A92556; WUID:87008488; PMID:3759943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-97, 1', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
A; Residues: 1-97, 'I', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', 3320-3426, 'T', 3428-
A; Residues: 1-97, 'I', 99-328, 'V', 330-644, 'I', 646-918, 'P', 920-3318, 'D', '3320-3426, 'T', 3428-
A; Residues: 1-97, 'I', 18-30-610, 'NID:917883; PIDN:AAA35549.1; PID:9178804
A; Note: a total of 2366 residues were confirmed by direct sequencing of tryptic peptides
R; Protter, A.A.; Hardman, D.A.; Sato, K.Y.; Schilling, J.W.; Yamanaka, M.; Hort, Y.J.; H'
Proc. Natl. Acad. Sci. U.S.A. 83, 5678-5882, 1986
A; Title: Analysis of cDNA clones encoding the entire B-26 region of human apolipoprotein
A; Reference number: A24320; MUID:86287319; PMID:3461454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AMOLECULE LYPE: MRNA
A;Residues: 1-97,'I', 99-617,'A', 619-941,'YYIWSLPPKP', 951-1138,'PTGRLPNCFSNGLICYSLWLHSFQE
A;Cross-references: GB:M14081, ND:G17875; PIN:AAA51752.1; PID:G553189
R;Law, S.W.; Lackner, K.J.; Hospattankar, A.V.; Anchors, J.M.; Sakaguchi, A.Y.; Naylor, Proc. Natl. Acad. Sci. U.S.A. 82, 8340-8344, 1985
A;Title: Human apolipoprotein B-100: cloning, analysis of liver mRNA, and assignment of A;Reference number: A24684; MUID:86094221; PMID:3001697
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A; Residues: 485-617, 74, 619-1044 <LA2>
A; Residues: 485-617, 74, 619-1044 <LA2>
A; Crocker, A: A: B: GB: MI2480; NID: 9178791; PIDN: AAAS1751.1; PID: 9178792
R; Procter, A: A: Hardman, D: A: Schilling, J W.; Miller, J: Appleby, V.; Chen, G.C.; Kil-Proct. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
Proc. Natl. Acad. Sci. U.S.A. 83, 1467-1471, 1986
A; Title: Isolation of a cDNA clone encoding the amino-terminal region of human apolipopr
A; Reference number: A94088; MUID: 86149325; PMID: 3513177
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A;Residues: 1282-2731,2742-3290,'L',3292-3336,'N',3338-3948,'F',3950-3963,'Y',3965-4180,
A;Cross-references: GB:MI5421; NID:g178817; PIDN:AAA51758.1; PID:g178818
A;Cross-references: DA,; Protter, A.A.; Chen, G.C.; Schilling, J.W.; Sato, K.Y.; Lau, K.; Yamana
Biochemistry 26, 5478-5486, 1987
A;Title: Structural comparison of human apolipoproteins B-48 and B-100.
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A; Residues: 1-291 < PRO>
A; Cross-references: GB:M12681; NID:g178797; PIDN:AAAS1753.1; PID:g178798
A; Deeb, S.S.; Motulsky, A.G.; Albers, J.J.
Proc. Natl. Acad. Sci. U.S.A. 82, 4983-4986, 1985
A; Title: A partial CDNA clone for human apoliprotein B.
A; Reference number: A25774; MUID:85270450; PMID:3860836
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A,Residues: 709-791, 'SSSWKAASHGCPHSAGD',810-906 <DEE>
A;Residues: 709-791, 'SSSWKAASHGCPHSAGD',810-906 <DEE>
A;Cross-references: GB:K03175; NID:g178821; PIDN:AAA51759.1; PID:g178822
R;Carlsson, P.; Darnfors, C.; Olofsson, S.O.; Bjursell, G.
Gene 49, 29-51, 1986
A;Title: Analysis of the human apolipoprotein B gene; complete structure
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C; Species: Homo sapiens (man)
A; Species: Homo sapiens (man)
S; Ja572; 1987
A; Lide: DNA sequence of the human apolipoprotein B gene.
A; Recence number: A27850; MUD: 88003974; PMID: 3652907
A; Molecule type: DNA
A; Reference number: A27850; MUD: 88003974; PMID: 3652907
A; Molecule type: DNA
A; Reference number: A27850; MUPROT: P78482; UNIPROT: P7849; UNIPROT: Q9UMNO; UNIF
B; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
B; Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
A; Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A; Reference number: A25679
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C;Species: Macaca fascicularis (crab-eating macaque)
C;Species: Macaca fascicularis (crab-eating macaque)
C;Accession: 532802
C;Accession: 532802
E;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchic Biochim. Biophys. Acta 1086, 3328-334, 1991
A;Title: Apo B metabolism in the cynomiqus monkey: evidence for post-transcriptional re A,Reference number: 532802; MUID:92075708; PMID:1742325
A,Referus: preliminary
A,Molecule type: mRNA
A,Residus: 1-59 c PAPA
A,Residus: 1-59 c PAPA
A,Residus: 1-59 c PAPA
A,Cross-references: UNIPROFICI28473; EMBL:X15737; NID:938047; PIDN:CAA33755.1; PID:993012
                                C;Accession: AE1065
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Connerton, P.; Cronin, A.; Davis, R.M.; Pickard, D.; Wain, J.; Churcher, S.; Connerton, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Attle: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; WUID:21534947; PMID:11677608
A;Accession: AE1065
A;Accession: AE1065
A;Accession: presiminary
A;Molecule type: DNA
A;Residues: 1-1099 cPAR>
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C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
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Pred, No. 1e+02;
Orintable 0; Indels
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Best Local Similarity 100.
Matches 7; Conservative
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Matches 9; Conservative
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A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free sn R;LeBoeuf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. FEBS Lett. 170, 105-108, 1984
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A, Molecule type: protein
A, Residues: 873-892, Kr, 894-896 < LE1>
A, Accession: A22006
A, Molecule type: protein
A, Residues: 873-892, Kr, 894-896 < LE1>
A, Accession: B22006
A, Molecule type: protein
A, Residues: 313, L', 3115-1130, Kr, 3132-3133, 'P', 3135-3136, 'R' < LE2>
A, Accession: B22006
A, Molecule type: protein
A, Residues: 3113, L', 3115-1130, 'R', 3122-3133, 'P', 3135-3136, 'R' < LE2>
R, Blackhart, B.D.; Ludwig, E.M.; Pierotti, V.R.; Caiati, L.; Onasch, M.A.; Wallis, S.C., J. Biol. Chem. 261, 15564-15367, 1986
A, 71tle: Structure of the human apolipoprotein B gene.
A, Reference number: A92564; MUID:87057153; PMID:2946672
A, 71tle: Studies on the organization of the human apolipoprotein B 100 gene.
R, Wagener, R.; Pitzner, R.; Stoffel, W.
Biol. Chem. Bope-Seyler 368, 419-425, 1987
A, 71tle: amontation; gene structure
R, Weisgraber, K.H. Rall Jr., S.C.
J. Biol. Chem. 262, 11097-11103, 1987
A, 71tle: Human apolipoprotein B-100 heparin-binding sites.
A, Reference number: A92605; MUID:87280197; PMID:3301850
A, Contents: amontation; heparin binding protein.
A, Reference number: A92605; MUID:87280197; PMID:307360
A, Contents: amontation; calcium binding protein.
A, Reference number: A92605; MUID:87280197; PMID:307360
A, Contents: amontation; calcium binding protein.
A, Reference number: A92605; MUID:8824245; PMID:307360
A, Contents: amontation; calcium binding protein.
A, Reference number: A9128, MUID:8624245; PMID:3841204
A, 71tle: Apolipoprotein B is a calcium binding protein.
A, Reference number: A918826, A11tle: Molecular cloning of human apolipoprotein B cDNA.
A, Reference number: A91868, A11tle: Molecular cloning of human apolipoprotein B cDNA.
A, Reference number: A91178; MUID:809360; PMID:3841204
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C;Spacession: B95329
R;Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; Bow
; Kalman, S.; Keating, D.H.; Pallm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K.C
Proc. Natl. Acad. Sci. U.S.A. 98, 9883-9888, 2001
A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium melilor
A;Reference number: A95262; MUID:21396509; PMID:11481432
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A;Accession: B95329
A;Status: preliminary
A;Accoule type: DNA
A;Accoule type: DNA
A;Couleule type: DNA
A;Couleule type: DNA
A;Couleule type: DNA
A;Cross-references: UNIPROT:Q92ZE8; GB:AE006469; PIDN:AAK65196.1; PID:g14523642; GSPDB:A;Cross-references: UNIPROT:Q92ZE8; GB:AE006469; PIDN:AAK65196.1; PID:g14523642; GSPDB:A;Carlort, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler
Bela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure
                                           А;Ассеввіол: А35783
A;Molecule type: protein
A;Residues: 28-41;76-97,'I',99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-
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A;Reference number: A22006; MUID:84208786; PMID:6373369
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Pred. No. 4.7e+02;
0; Mismatches 0;
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Best Local Similarity 90.0
Matches 9, Conservative
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Ajaccession: A29671
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Ajaccession: 1671-2323 'PYW', 2327-2352,'H',2354-2398 cHAR>
Ajaccession: A2937 'Sylvatt, Nal.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.; Atherosclerosis 58, 277-289, 1985
Ajaccession: A2928 cHO, Ajaccession: A2572 choracterization of a human apolipoprotein B 100-spectore number: A25572 chulb: 87076044; PMID:3024665 choracterization cho
number: A29671; MUID:88050832; PMID:3676265
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A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0724
C;Superfamily: Chlamydia pneumoniae hypothetical protein CPn0724
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41 TKATRRGLR 49
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() Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
() Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
() Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
() Pate: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change 09-Jul-2004
() Accession: D72044; C81621
() Rature Genet: 21, 385-389, 1999
() Rature Genet: 21, 385-389, 1999
() Rature Genet: 21, 385-389, 1999
() Arginan, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
() Rature Genet: 21, 385-389, 1999
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() Rature Genet: 21, 385-389, 1999
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Species: Charson #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: A86581
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
R;Shirai, Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-274 <STO>
A;Residues: 1-274 <STO>
A;Cross-references: UNIPROT:092711; GB:BA000008; NID:g8979096; PIDN:BAA98931.1; GSPDB:GN
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti. A;Reference number: A96039; MUID:21368234; PMID:11474104 C;Contents: annotation C;Genetics:
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C;Superfamily: Chlamydia pneumoniae hypothetical protein CPn0724
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Best Local Similarity 75.0
Matches 6; Conservative
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106 KLTRRGLR 113
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41 TKATRRGLR 49
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Best Local Similarity
Matches 6; Conserv
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A;Genome: plasmid
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Glycerol dehydrogenase homolog lin1848 [imported] - Listeria innocua (strain Clip11262)
CiSpecies: Listeria innocua
CiSpecies: Listeria innocua
CiSpecies: Listeria innocua
CiAccession: AG1663
RiGlaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker.
Joninguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
Science 294, 849-852, 2001
Alauthors: Kreft, J.; Kunn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
A; Hitle: Comparative genomics of Listeria species.
A; Reference number: AB1077; MUID: 21537279; PMID: 11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1.368 <GLA>
A;Cross-references: UNIPROT:Q92AS1; GB:AL592022; PIDN:CAC97079.1; PID:gL6414350; GSPDB:C
A;Experimental source: strain Clip11262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-368 <GLA>
A;Cross-references: UNIPROT:Q8Y6F0; GB:NC_003210; PIDN:CAC99815.1; PID:g16411191; GSPDB.
A;Experimental source: strain EGD-e
C;Genetics:
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C;Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
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C;Superfamily: Glycerol dehydrogenase; lactaldehyde reductase homology
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       Score 33; DB 2; Length 274; Pred. No. 44; 2; Mismatches 1; Indels
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Pred. No. 58;
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Query Match
Best Local Similarity 66.7%;
Matches 6; Conservative
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us-09-823-418-13.rpr

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hypothetical protein CC2774 [imported] - Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cispecies: Caulobacter crescentus
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
Ciscossion: F87592
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
I. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
A;Tile: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; WUID:21173698; PMID:11259647
A;Accession: F87592
A;Accession: Preliminary
A;Residues: 1-514 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9A4Q6; GB:AE005673; NID:g13424372; PIDN:AAK24738.1; GSPDB:<
C;Genetics:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: T05005
R;Bevan, M.; Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, April 1998
A;Reference number: Z15394
A;Accession: T05005
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R;Thomson, K.G.; Thomas, J.E.; Dietzgen, R.G.
Bjant Mol. Biol. 38, 461-465, 1998
A;Title: Retrotransposon-like sequences integrated into the genome of pineapple, Ananas A;Reference number: Z16184; MUID:98418625; PMID:9747853
A;Accession: T07863
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A;Molecule type: DNA
A;Residues: 1-871 <THO>
A;Residues: 1-871 <THO>
C;Genetics:
C;Genetics:
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C;Species: Ananas comosus (pineapple)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
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A,Residues: 1-633 <BEV>
A;Residues: 1-633 <BEV>
A;Cross-references: UNIPROT:065655; EMBL:AL022605
A;Experimental source: cultivar Columbia; BAC clone T19P19
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Pred. No. 78;
0; Mismatches
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95;
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Pred. No. 95;
0; Mismatches
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77.8%;
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87.5%;
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A;Introns: 385/1; 448/1; 498/3
A;Note: T19P19.70
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Best Local Similarity 87.5
Matches 7; Conservative
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Best Local Similarity 77.8
Matches 7; Conservative
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                                                                                                                                                                                                                                                                                                        hypothetical protein BH4041 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Date: 0.1Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84155
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000
A;Riferce Acids Res. 28, 4317-4331, 2000
A;Reference number: A83650; MUD:20512582; PMID:11058132
A;Accession: A84155
A;Accessi
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A; Residues: 1-451 - KUR.
A; Residues: 1-451 - KUR.
A; Residues: 1-61 - KUR.
A; Cross-references: UNIPROT: 092WV7; GB: AL591985; PIDN: CAC48622.1; PID: G15140094; GSPDB: G
A; Experimental source: strain 1021, megaplasmid pSymB
R; Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A; Atthors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A; Reference number: A96039; MUID: 21368234; PMID: 11474104
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C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: F95869
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endc A;Reference number: A95842; MUD:21395508; PMID:11481431
A;Status: preliminary
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A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH4041
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Pred. No. 66;
2; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
   7; Conservative
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TRITKRGRK 347
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hypothetical protein SC5F2A.18 - Streptomyces coelicolor C.Species: OS-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Ju1-2004 C.Accession: T35260
R;Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Rolliver, K.; Harris, Data Library, April 1999
A;Reference number: Z21573
A;Accession: T35260
A;Accessi
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A; Mobile element: retrotransposon deal
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272 TRLTHKGVK 280
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144 RLTRRGI 150
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Search completed: December 29, 2004, 12:39:08 Job time : 9.69318 secs

O8v6f0 listeria

Q91db7 streptomyce Q82cw6 streptomyce Q82cw6 streptomyce Q75tw9 bacillus fi Q75tm6 bacillus fi Q75tm1 bacillus al Q75tx1 bacillus ha Q75tx3 bacillus ha Q75tx6 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha Q75tx7 bacillus ha

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MEDLINE-201319; PubMed=12730200;

Parschat K., Hauer B., Kappl R., Kraft R., Huettermann J., Fetzner S.;

"Gene Cluster of Arthrobacter ilicis R.61a Involved in the Degradation of Quinaldine to Anthromilate. Characterization and Functional Expression of the Quinaldine 4-oxidase qoxLMS Genes.";

J. Biol. Chem. 278:27483-27494 (2003).

BMBL; AJS37473; CAD61041.1;

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:001601; P:transporter activity; IEA.

GO; GO:000810; P:transport: IEA.

InterPro; IPR007114; MFS.

PROSITE; PSSO850; MFS; 1.

SEQUENCE 423 AA; 43696 MW; BB11CBADA85DF241 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Arthrobacter ilicis.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Micrococcineae; Micrococcaceae; Arthrobacter.
NCBI_TaxID=43665;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
101-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical cytosolic protein.
Name=FNV0795;
Fusobacterium nucleatum subsp. vincentii ATCC 49256.
Bacteria; Fusobacteria; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                           01-007-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 24;
2; Mismatches
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0816F0
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Best Local Similarity 77.8%;
Matches 7; Conservative
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207 TRLTKQGLK 215
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SEQUENCE FROM N.A.
STRAIN=ATCC 49256;
 STRAIN-Rue61a;
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   Q7P2I3;
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Q9phw2 xanthomonas
Q71yt1 listeria mo
Aat04533 listeria
Q92as1 listeria in
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salmonella
yarrowia li
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gallus gall
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homo sapien
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homo sapien
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073uw5 mycobacteri
Aa805799 mycobacte
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                                                                                                                    (without alignments)
98.508 Million cell updates/sec
                                                                                                     December 29, 2004, 12:13:11 ; Search time 52.5682 Seconds
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Q740b8 myc
Aa803750 m
Q98hm9 rhin
Q7rz12 neu
Q9871b neu
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Q8871b neu
Q8871b neu
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Q13788
P04114
Q7z600
Q98nd4
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               GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q92ZE8
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 200000000
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SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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Karpatral V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A., Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T., Haselkorn R., Overbeek R., Kyrpides N.; Submitted (JAN-2003) to the EWBL/GenBank/DDBJ databases.

-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lykidis A.,
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Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
Fusobacterium.
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                                                                                                    preliminary data.
EMBL; AABF01000083; EAA23797.1; -.
Hypochetical protein.
SEQUENCE 503 AA; 57362 MW; 70DE5CADE118516C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel. 21, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                          Score 36; DB 2;
Pred. No. 49;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 2;
Pred. No. 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical cytosolic protein.
OrderedLocusNames=FN1121;
                                                                                                                                                                                            81.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.8 Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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126 TRLERRGIK 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRLERRGIK 134
                                                                                                                                                                                                                                                           1 TRLTRRGLK 9
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                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=76856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPA (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002
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01-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126
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                                                                                                                                                                                                                                                                                                                                                                                                OBREI1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8QHI6;
Q8QHI6;
                                                                                                                                                                                                                                                                                                                                                                                Q8REI1
                                                                                                                                                                                                                           Matches
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RESIDENCE FROM N.A.

RECONTINE_2518L/6J; TISSUE=Breast tumor, and Heart;

RECONTINE_25184681; PubMed=12466651; DOI=10.1038/nature01266;

RA MINIME_25184681; PubMed=12466651; DOI=10.1038/nature01266;

RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yamanaka I., Rayosawa H., Radarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,

RA Baldarelli R., Hill D.P. Bult C., Hume D.A., Quackenbush J.,

RA Schriml L.M., Kanapin A., Mateuda H., Batalov S., Baisel K.W.,

Bake J.A., Bradt D., Brusic V., Chothla C., Corbani L.B., Cousins S.,

RA Gassterland T., Gariboldi M., Glssi C., Godzik A., Gough J.,

Girmmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

RA Anata A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

Magdott D.R., Maltels L., Marchionni L., McKenzie L., Miki H.,

RA Konagaya A., Kurochkin I.V., Lee Y., Lehhard B., Lyons P.A.,

Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Milming L.G., Wyushaw-Boris A., Yanagisawa M., Yang I., Yang I.,

RA Sarado R., Washar T., Konno H., Nakamura M., Sakaume N.,

RA Miyazaki R., Rawi K., Kawai J., Alzawa R., Sakaume N.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Sanulshi A., Schaino M., Waterston R., Ishii Y., Itoh M., Sagawa J.,

RA Sanulshi A., Sakaki K., Sasaki D., Shinagawa A.,

RA Sanulshi A., Sakaki K., Sasaki D., Shinagawa A.,

RA Sanulshi A., Sakaki Y.,

RA Sanulshi A., Sakaki Y.,

RA Sanulshi A., Shinagawa A.,

RA Sasaki D., Shinagawa A.,

RA Sasaki Y.,

RA Sasaki D., Shinagawa A.,

RA Sasaki D., Shinagawa A.,

RA Sasaki D
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"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gарв
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PRT; 400 AA.

98BLD6; QRSSH7; Q8VDT7; Q922NS;
05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
F-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Musinae, M
                                                          Das T., Purkayastha Mukherjee C., D'Angelo J., Weir M.; "A conserved F-box gene with unusual transcript localization."; Dev. Genes Evol. 212:134-140(2002).
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                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Das T.K., Purkayastha-Mukherjee C., D'Angelo J., Weir M.
Submitted (BEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF467464, AAL75968.1; -.
InterPro; IPR007611; LRR.
InterPro; IPR007089, IRR.
Pfam; PF00560; LRR; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 AA; 20629 MW; 21702832DA5CE865 CRC64;
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MEDLINE=21972450; PubMed=11976951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=Fbx114; Synonyms=Ppa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TRLTRRGLK 9
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FXLE HUMAN
                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Strausberg R.L., Zeeberg B.S., Wagner L., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Zeeberg B., Buercw K.H., Schaefer C.F., Bhat N.K., A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Didchenko L., Marusiana K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rotherch A., Schain J.B., Jones S.J.M., Marra M.A., Schaiu D.E., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                           -> F (in Ref. 2; AAH21329).
E0B297E4B4F83C22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    conjugation pathway.
                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB
Pred. No. 63;
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F-box.
LRR 1.
LRR 2.
LRR 3.
LRR 4.
LRR 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR007089; LRR cys.
InterPro; IPR008945; Skp1_Skp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AK084506; BAC39201.1; -. EMBL; BC006913; AAH021931.1; -. EMBL; BC021329; AAH21329.1; -. EMBL; AF467463; AAL75967.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE ]
Leucine-rich repeat; Repeat; U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43864 MW;
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66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001810; F-box. InterPro; IPR001611; LRR.
                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:2141676; Fbx114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00646; F-box; 1.
Pfam; PF00560; LRR; 6.
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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REPEAT
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Gaps

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0; Indels

3, Mismatches

Conservative

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**X TISUBLE-LUB | X-1. 
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                                                                                                                                                                                                            05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
R-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).
--- SIMILARITY: Contains 1 F-box domain.
--- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
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                                                                                                                                                                   418 AA
                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F-box.
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LRR 2.
LRR 3.
LRR 4.
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PROSITE; PS50181; FBOX; FALSE NEG.
Leucine-rich repeat; Ubl c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; BC028132; AAH28132.1; -.
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InterPro; IPR001611; LRR.
InterPro; IPR007089; LRR_cys.
Pfan; PP00646; F-box; 1.
Pfan; PF00560; LRR; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genew; HGNC:28624; FBXL14
                                                                                                                                                                   STANDARD;
                           367 TRITKRGLE 375
1 TRLTRRGLK 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
170
203
254
                                                                                                                                                                                                                                                                                                                                       Name=FBXL14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE=Lung
                                                                                                                                                                   FXLE HUMAN OBN1\overline{E}6;
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REPEAT
REPEAT
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                                                                                                                                                                                                                                                                                                   Pearce A.,
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the small GTPase superfamily. Rho family.
                                                                                                                                                                                                                    Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB 1; Length 192;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                       16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Ras-related C3 botulinum toxin substrate 4 (p21-Rac4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 192 AA; 21383 MW; 09CSDFE64C8E6053 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                192 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 777.34; CCCC No. 47; Best Local Similarity 100.0%; Pred. No. 47; Matches 7; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AL022576; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genew; HGNC: 31113; RAC4.
InterPro; IPR00180; GTPase_Rho.
InterPro; IPR001806; Ras trinsfrung.
InterPro; IPR00525; Small_GTP.
Pfam; PF00071; Ras; 1.
PRINTS; PR00449; RASTRNSFRMNG.
SMART; SM0174; RHO; 1.
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01-OCT-2001 (TrEMBLrel. 18, Last seqnol-OCT-2003 (TrEMBLrel. 24, Last annomall2796 protein.
OrderedLocusNames=mll2796;
Rhizobium loti (Mesorhizobium loti).
                                                                                            STANDARD;
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               243 TRLTRRG 249
                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HSSP; P15154; 1HH4.
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
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                                                                                           RAC4 HUMAN
095916:
                                                                                                                                                                                       Name=RAC4;
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                                                                          RAC4 HUMAN
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Li L., Bannantine J., Zhang Q., Amonsin'A., Alt D., Kapur V.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AE01732; AAS03750.1; -.
Complete proteome; Hypothetical protein.
SEQUENCE 581 AA, 61736 MW, 408204896800 CPC61.
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                                                                                                                                                                                                                                                                                                                                                 Mycobacterium paratuberculosis.
Bacteria; Actinobacteria; Actinobacteriles;
Corymebacterineae; Mycobacteriaese; Mycobacterium;
Mycobacterium avium complex (MAC).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
NCBI_TaxID=1770;
                                                              79.5%; Score 35; DB 1; Length 418; 66.7%; Pred. No. 66; 1, Wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79.5%; Score 35; DB 2; Length 581; 100.0%; Pred. No. 95; atlve 0; Mismatches 0; Indels
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                                 5779961C8177779F CRC64;
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                                                                                                                                                                                                                                 0740B8 PRELIMINARY; PRT; 581 AA. 0740B8; 05-JUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Hypothetical protein.
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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79.5%; Score 35; DB 2
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches
   LRR 5.
LRR 6.
                                45886 MW;
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                                           Query Match
Beet Local Similarity 66.70,
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367 TRITKRGLE 375
                                                                                                                            1 TRLTRRGLK 9
331 3
357 3
418 AA;
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243 TRLTRRG 249
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MAP1433C.
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               REPEAT
SEQUENCE
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Matches
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"The Genome Sequence of the Filamentous Fungus Neurospora
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Name=B8G12.280;
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63 RITRRGLR 70
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A Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
Belking T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
A Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
A Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
A Kamal M., Kamvyseelis M., Maucell E., Bielhe C., Rudd S., Frishman D.,
Krystofova S., Rasmussen C., Maczenberg R.L., Perkins D.D., Kroken S.,
Cogoni C., Macino G., Catchedide D., Li W., Pratt R.J., Osmani S.A.,
DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
Yarden O., Plamann M., Seiler S., Dunlap J., Refteng M.,
Natvig D.O., Alex L.A., Mannhaupt G., Bibole D.J., Freitag M.,
Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
                                                                                                    Kaneko T., Nakamura Y., Sato S., Asamizu B., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizobium loti (supplement).";
                                                                                                                                                                                                                                                                                       Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           321 AA; 34893 MW; C6PB1DA0CC1D73D8 CRC64;
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01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.3%; Score 34; DB 2;
100.0%; Pred. No. 82;
iive 0; Mismatches (
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EMBL; AP003000; BAB49837.1; -.
GO; GO:0016787; F:hydrolase activity; IEA
                                                                                                                                                                                                                                                                           MEDLINE=21082930; PubMed=11214968;
                                                                         STRAIN=MAFF303099;
MEDLINE=21082936; PubMed=11214974;
              Phyllobacteriaceae; Mesorhizobium
NCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro, IPR004843, M-pesterase.
Pfam, PF00449, Metallophos, 1.
Complete proteome.
SEQUENCE 321 AA, 34893 MW, C6F
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Best Local Similarity 100.
Matches 7; Conservative
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289 RLTRRGL 295
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                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                            STRAIN=MAFF303099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
Nature 0:0-0(2003).
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 34; DB 2; Length 369; 75.0%; Pred. No. 96; ive 2; Mismatches 0; Indels
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX294027; CAD71088.1; -.
GO; GO:0004497; Fromonoxygenase activity; IEA.
GO; GO:0006725; P:aromatic compound metabolism; IEA.
GO; GO:0006118; P:electron transport; IEA.
                                                                             Preliminary data.

EMBL, ABRX0100721, EAA28183.1, -...
GO, GO:0004971, F.moncoxygenase activity, IEA.
GO, GO:0006725; P:aromatic compound metabolism; IEA.
GO, GO:0006118; P:electron transport; IEA.
InterPro; IPR000733; Flav moncoxygenase.
InterPro; IPR003042; Rng_mnoxygenase.
PETMI; PR01360; Moncoxygenase, 1.
PRINTS; PR01420; RNGMNOXGNASE.
SEQUENCE 369 AA, 40627 NW; D53DE9368557BE47 CRC64;
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Last annotation update)
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10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2004 (Rel. 44, Last annotation update)
Cobyrinic acid A,C-diamide synthase.
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InterPro; IPR003042; Rng_mnoxygenase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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Best Local Similarity 75.v-
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 75.0
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                                                                                                                                                                                                                                                                                              Res. 77:31-38(2000).

FINCTION: Responsible for the amidation of carboxylic groups at POSITION A and C of either cobyrinic acid or hydrogenobrynic acid. NH(2) groups are provided by glutamine, and one molecule of ATP is hydrogenolyzed for each amidation (By similarity).

PATHWAY: Cobalamin blosynthesis.

SIMILARITY: Belongs to the cobB/cobQ family. CobB subfamily.
                                                                                                                           STRAINMARF20309;
MEDLINE-210809;
MEDLINE-2108230; PubMed=11214968;
MEDLINE-2108230; PubMed=11214968;
MEDLINE-2108230; PubMed=11214968;
Matanabe A., Ideauwa K., Sato S., Asamoto S.,
Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
Takeuchi C., Yamada M., Tabata S.,
"Complete genome structure of the nitrogen-fixing symbiotic bacterium
DNA Res. 7:331-338(2000).
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MEDLINE=88070650; PubMed=2825356;
Hirai H., Maru Y., Hagiwara K., Nishida J., Takaku F.;
"A novel putative tyrosine kinase receptor encoded by the eph gene.";
Science 238:1717-1720(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | PR1; 976 AA. | PR10MAN STANDARD; PR1; 976 AA. | PP1709; Q15405; Q15405; Q15405; Q1991 (Rel. 18, Created) | O5-JUL-2004 (Rel. 44, Last sequence update) | O5-JUL-2004 (Rel. 44, Last annotation update) | Ephrin type-A receptor 1 precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor EPH). | Name=EPHA1; Synonyms=EPH71, EPH; Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Name=cobB; OrderedLocusNames=mlr1387;
Malzoblum lot1 (Mesorhizoblum lot1).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.3%; Score 34; DB 1; Length 439; 100.0%; Pred, No. 1.26+02; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGRRAMS; TIGRO0379; cobB; 1.
Cobalamin biosynthesis; Complete proteome.
SEQUENCE 439 AA; 45879 MW; DCFB9F997D2948B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A.
MEDLINE=99299440; PubMed=10369740;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAMAP; MF 00027; -; 1. Interpro; IPR002586; CbiA P. Interpro; IPR004444; CbiA synth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP002997; BAB48773.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01656; CbiA; 1.
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28 LTRRGLK 34
                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tuzi N.L.;
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-- PUCTION: Receptor for members of the ephrin-A family. Binds with a low affinity to ephrin-A1.
-- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
-- SUBCELLUIAR LOCATION: Type I membrane protein.
-- SUBCELLUIAR LOCATION: Type I membrane protein.
-- TISSUE SPECIFICITY: Overaxpressed in several carcinomas.
-- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor aubfamily.
-- SIMILARITY: Contains 2 fibronectin type III domains.
-- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Owshalimpur D., Kelley M.J.;
"Genomic structure of the EPHA1 receptor tyrosine kinase gene.";
Mol. Cell. Probes 13:169-173(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human chromosome 7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M18391; AAA36747.1; ALT SEQ.
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TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The DNA sequence of human
Nature 424:157-164(2003).
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MEDLINE-21534947; PubMed=11677608; DOI=10.1038/35101607; MEDLINE-21534947; PubMed=11677608; DOI=10.1038/35101607; MEDLINE-21534947; PubMed=11677608; DOI=10.1038/35101607; Milline-115. Milling-115. Mil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIR=1242 / Arcc 700931,
MEDLINE=2253136; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
and C.Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CT18.
                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                             01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein STY4851.
OrderedocusNames=STY4851, t4545;
Salmonella typhi.
                                                                                                                                                                                                                                                            Enterobacteriaceae; Salmonella
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             NCBI_TaxID=601;
      Q8Z0Z1; Q7C4Y0;
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RECOOM; PRO01495; Ephrin_receptor; 1.

RECOOM; PRO01495; Ephrin_receptor; 1.

REMART; SM00615; EPH 15d; 1.

REMART; SM00150; FYER 1.

REMART; SM00150; FYER 1.

REMART; SM00150; FYER 1.

REMART; SM00150; FYER 1.

REMART; SM0019; FYER 1.

REMART; SM00110; FROTEIN KINASE APP; 1.

REMOSITE; PS00110; PROTEIN KINASE DOM; 1.

REMOSITE; PS00110; RECEPTOR_TYR KIN V. 1.

REMOSITE; PS00190; RECEPTOR_TYR KIN V. 1.

REMOSITE; PS00191; RECEPTOR_TYR KIN V. 2.

REMOSITE; PS00191; RECEPTOR_TYR KIN V. 1.

REMOSITE; PS00191; RECEPTOR_TYR KIN V. 1.

REMOSITE; PS00191; RECEPTOR_TYR KIN V. 2.

REMOSITE; PS00191; RECEPTOR_TYR KIN V. 1.

REMOSITE; PS00191; REMOSITE; PS001
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Phosphotyrosine (by autocatalysis)
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ATP (By similarity).
ATP (By similarity).
By similarity.
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Cys-rich.
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Fibronectin type-III 2.
Protein kinase.
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                                                                                                                    InterPro; IPR001245; Tyr pkinase.
InterPro; IPR001245; Tyr pkinase_AS.
InterPro; IPR001426; Ykase receptorV.
Pfam; PF01404; Ephrin lbd; I.
Pfam; PF000641; fn3; 2.
Pfam; PF00069; Pkinase; I.
IPR008957; FN III-like.
IPR008979; Gal bind like.
IPR000719; Prot_kinase.
                                                                                                   SAM.
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Best Local Similarity 100.
Matches 7; Conservative
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DOMAIN
TRANSMEM
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CARBOHYD
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                                                                                                                                77.3%; Score 34; DB 2; Length 1099; 100.0%; Pred. No. 3.2e+02; ive 0; Mismatches 0; Indels
J. Bacteriol. 185:2330-2337 (2003).

EMBL; AL627283; CAD06970.1; -.

EMBL; AR016849; AAO71983.1; -.

COMDlate proteome; Hypothetical protein.

SEQUENCE 1099 AA; 125223 MW; 6131DD4E8ABSF6A5 CRC64;
                                                                                                                                                                                                                                                                                                                                   Search completed: December 29, 2004, 12:37:38 Job time : 54.6793 secs
                                                                                                                                                                              7; Conservative
                                                                                                                                                            Local Similarity
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PRT; 1099 AA.

PRELIMINARY;

Q8Z0Z1 ID Q8Z0Z1 RESULT 15

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December 29, 2004, 12:10:41 ; Search time 54.9205 Seconds (without alignments) 58.786 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1 TRLTKRGLK 9
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geneseqp2001s:*
geneseqp2002s:*
geneseqp2003s:*
geneseqp2003bs:* A_Geneseq_23Sep04:* Database :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lon	Apo-B100	Apo-B100	Apo-B100	Human PMM	Human NOV	Zea mays	Thermococ	Xanthomon	Protein e	GAP prote	Apo-B100	Apo-B100	Apo B bin	Apo B 100	Apolipopr	ApoB-100	Heparin b	Apo B 100	Apo B 100	Human apo	Nucleic a	Human apo	Nucleic a	Peptide #	Human liv
Description	Aay30695	Aay30694	Aay30696	Abr43240	Abg97506	Aag40845	Adn47506	Adg30649	Abu48780	Aar59926	Aay30689	Aay30688	Aaw57205	Aaw57207	Aaw41261	Aaw96892	Abj37575	Aaw57208	Aaw57209	Aae14541	Aaw96876	Aaw64587	Aaw96845	Abb37687	Abg52504
ID	AAY30695	AAY30694	AAY30696	ABR43240	ABG97506	AAG40845	ADN47506	ADG30649	ABU48780	AAR59926	AAY30689	AAY30688	AAW57205	AAW57207	AAW41261	AAW96892	ABJ37575	AAW57208	AAW57209	AAE14541	AAW96876	AAW64587	AAW96845	ABB37687	ABG52504
DB	8	N	N	9	ഹ	٣	œ	7	9	~	N	~	N	~	N	~	9	N	~	ß	~	N	~	4	4
* Query Match Length DB	6	6	6	404	548	146	238	335	840	3079	10	10	11	13	15	15	20	22	22	34	36	37	51	343	343
% Query Match	100.0	93.2	86.4	86.4	86.4	79.5	77.3	77.3	77.3	77.3	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1	76.1
Score	44	41		38	38	35	34	34	34	34	33.5	33.5	33.5	33.5	•			33.5	٠	33.5	ω,	m,	33.5	٠	33.5
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Aar72704 Human apo Aar34031 Sequence Adj57400 Human apo Aay31237 Human apo Aaw41262 Apolipopr Aaw96826 Amino aci Aau99991 Human apo Add48677 Human apo Add48677 Human apo Abu79140 Apolipopr Adf43408 Apolipopr Adf43408 Apolipopr Adf18871 Human apo	
AAR72704 AAR34031 ADU57400 AAY31237 AAW41262 AAW96836 AAW98811 ADD48677 AAO15893 ABR402533 ABR40253 ABR403408 ADF43408	AD033445 AD033447 AD033447 AAU33184 AAY30699 AAY30697 AAE12587
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ALIGNMENTS

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Sequence 9 AA;

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atherosclerotic regions. Thus the assays may be used to determine whether sparticular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
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                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                                                     Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                             Apo-B100 derived peptide showing a proteoglycan receptor mutation.
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                                                                                            Query Match
100.0%; Score 44; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
  identify compounds which result in
                                                                                                                                                                                                               AAY30694 standard; peptide; 9 AA.
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                                                                                                                                                      TRLTKRGLK
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   used to
                                                                         Sequence 9 AA;
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                                                                                                                                                                                                                                                                                                                                    Synthetic.
Homo sapiens
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Best Local Similarity 77.8 Matches 7; Conservative
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                                                                              AAY30582-Y30700 represent apo-Blo0 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which receptor mutations. They were created to identify compounds which which method comprises detecting compounds which affect to 3367 of apoBlo0. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding such compounds can be used to atheroselerosis. The transgenic non-human animals and mammals which express human apo-Blo0 can be used an in vivo model system for the express human apo-Blo0 can be used an in vivo model system for the compounds which medulate atheroselerosis and/or LDL-PG binding. They can also be used to identify compounds which result in an increase in a particular food or drug compounds which result in an increase in a particular food or drug composition tends to stimulate or inhibit the commation of atheroselerotic lesions. The polynuclectides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
Claim 17; Page 57; 70pp; English.
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Gaps

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0; Indels

Score 38; DB 2; Length 9; Pred. No. 1.7e+06; 2; Mismatches 0; Indels

86.4%;

1 TRLTKRGLK 9

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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which are deceptor mutations. They were created to identify compounds which modulate atheroselerosis. The peptides are derived from amino acids 3358 to 3367 of apobl00. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding without inhibiting LDL receptor binding. Such compounds can be used to atheroselerosis. The transpension of atheroselerosis and mammals which express human apo-B100 can be used as an in vivo model system for the compounds which modulate atheroselerosis and/or LDL-PG binding. They can be used to identify compounds which result in an increase in a particular food or drug composition tends to etermine whether formation of atheroselerosis and/or LDL-PG binding. They can aparticular food or drug composition tends to etermine whether formation of atheroselerosic lesions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atheroselerosis in an animal or mammal
                                                            ô
                                                            Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                                                                                                                                            Apo-B100; proteoglycan receptor mutation, atherosclerosis,
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                         Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                            ;
                 Score 41; DB 2; Length 9;
Pred. No. 1.7e+06;
1; Mismatches 0; Indels
                                                     1; Mismatches
                                                                                                                                                                                               AAY30696 standard; peptide; 9 AA.
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                    93.2%;
88.9%;
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Query Match
Best Local Similarity 88.95,
....a 8; Conservative
                                                                                                                                                                                                                                                             17-NOV-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Innerarity TL, Boren JOS;
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                                                                                                    WPI; 1999-551509/46.
                                                                                 1 TRLTKRGLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                           WO9946598-A1
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                                                                                                                                                                                          antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective; AIDS; cerebroprotective; anti-HIV; antiallergic; antiinflammatory; cancer; thyromimetic; gene therapy; cell proliferative disorder; atherosclerosis; neurological disorder; epilepsy; Huntington's disease; stroke; allergy; immune disorder; inflammatory disorder; developmental disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human protein modification and maintenance molecules (PMMM), useful for diagnosing, treating and preventing diseases or conditions associated with the aberrant PMMM expression e.g. cancer, AIDS, epilepsy, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Becha SD;
Khare R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC5959 to ACC59889 encode the human protein modification and maintenance molecule proteins given in ABR43240 to ABR43270, designated PMMW-1 to PMMW-31 (I). (I) have cytostatic, antiatreriosclerotic, anticonvulsant, nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic, antiinflammatory and thyromimetic activities, and can be used in gene therapy. The PMMM polypeptides and polynucleotides are useful in diagnosing, treating and preventing diseases or conditions as sociated with the decreased expression or overexpression of PMMM, such as cell proliferative (e.g. cancer, atherosclerosis), neurological (e.g. epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AlDS, allergies) and developmental (e.g. hypothyroidism, Cushing's syndrome) disorders, or infections. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid
                                                                                                                                                                              Human; protein modification and maintenance molecule; PMMM; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chawla NK, Warren BA, Tang YT, Elliott VS;
Li JX, Griffin JA, Gietzen KJ, Yang J, Lu DAM;
Duggan BM, Richardson TW, Lee SY, Ramkumar J,
M, Swarnakar A, Tran UK, Kable AE, Hafalia AJA,
                                                                                                                                                                                                                                                        hypothyroidism; Cushing's syndrome; infection.
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                                                                           ABR43240 standard; protein; 404 AA
                                                                                                                                                      Human PMMM-1 protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                               20010S-0324134P

20010S-0327233P

20010S-034369B-

20010S-034368P-

20010S-03488B7P

20010S-0332423P-

20010S-033445P-

20010S-033423P-

20010S-033423P-

20010S-033423P-

20010S-0337451P-

20020S-0351928P-
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                                                                                                                             (first entry)
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N-PSDB; ACC59959.
TRLTRKGLK
                                                                                                                                                                                                                                                                                                          WO2003025131-A2.
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                                                                                                                                                                                                                                                                                  Homo sapiens.
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09-NOV-2001;
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                                                                                                                           07-JUL-2003
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Marquis JP,
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                            compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polypucleotide and compounds that specifically bind to or medulate the activity of the polypeptide. The microarray is useful in monitoring or measuring protein-protein
PMMM. The PMMMs or their fragments are useful in screening
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                                                                                                                                                   interactions, drug-target interactions, and gene expression profiles
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Pred. No. 20;
2; Mismatches
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12-MAR-2001; 200105-027525F

13-MAR-2001; 200105-0275601P

14-MAR-2001; 200105-0275601P

20-MAR-2001; 200105-0275000P

20-MAR-2001; 200105-0277339F

21-MAR-2001; 200105-0277338P

21-MAR-2001; 200105-0277338P

22-MAR-2001; 200105-0277338P

23-MAR-2001; 200105-0277338P

24-MAR-2001; 200105-0279338P

27-MAR-2001; 200105-0279336P

28-MAR-2001; 200105-0279338P

29-MAR-2001; 200105-0279338P

20-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P

21-MAR-2001; 200105-0279338P
                                                                                                                                                                                                                                                                     86.4%;
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Best Local Similarity 77...
                                                                                                                                                                                                                                                                                                                                                                                                                                                     367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOVX25 protein.
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                                                                                                                                                                                                               Sequence 404 AA;
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99US-0121825P.
99US-0123180P.
99US-0123548P.
99US-0125788P.
99US-0126784P.
99US-0126782P.
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99US-0128714P.
99US-0129845P.
99US-0130077P.
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990S-0132486P-
990S-0132486P-
990S-0132487P-
990S-0132863P-
990S-0134218P-
990S-0134219P-
990S-013421P-
990S-013421P-
990S-013421P-
990S-013421P-
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9905-0136629P

9905-0136392P

9905-0137528P

9905-0137528P

9905-0137528P

9905-0137528P

9905-0137528P

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9905-0139453P

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9905-0139455P

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9905-0139455P
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99US-0139463P.
99US-0139750P.
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                 05- MAR-1999;
09-MAR-1999;
23-MAR-1999;
29- MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
21-APR-1999;
21-APR-1999;
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28-APR-1999;
30-APR-1999;
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05-MAY-1999;
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07-MAY-1999;
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14-MAY-1999;
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24-MAY-1999;
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       The present invention relates to a new polypeptide (Novx). The Novx colypeptide, nucleic acid and antibody are useful in the manufacture of a medicament for treating a syndrome associated with a human disease, confederably a NovX-associated disorder. The NovX nucleic acids, or preferably a NovX-associated disorder. The NovX nucleic acids, or dispeptides and antibodies are useful for treating, preventing or dispensing diseases uch as cancers, Hodgkin disease, Von Hippel-Lindau syndrome, Alzheimer's disease, stroke, tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral hypercalcaemia, Parkinson's disease, Huntington's disease, cerebral palay, epilepsy, Lesch-Nyhan syndrome, multiple sclerosis, ataxiactellangictusia, leukodystrophies, addiction, antiety, depression, pain, obesity, Crohn's disease, osteoporosis, inflammatory bowel disease, atherosclerosis, hypertension, scleroforma, hemophilia, diabetes, pancreatitis, autoimmune disease, infections, or graft-versus-host disease. The nucleic acids and scleroforman, and any also be used as targets for the identification of small complements, in gene therapy, in generation of antibodies that bind differentiation, cell proliferation, hematopolesis, wound healing and cimmunospecifically to NovX substances for use in therapeutic or immunospecifically to NovX substances for use in therapeutic or diagnostic methods. The nucleic acids are further used as hybridisation probes, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present amino acid sequence represents a human NoVX noterin of the invantion
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                                                                                                         New NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. diabetes, multiple sclerosis, atherosclerosis, cancer, infections, osteoporosis or parkinson's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
            Spytek KA, Vernet CA, Tchernev VI, Malyankar UM, Gerlach VL;
Li L, Zerhusen BD, Patturajan M, Gusev VY, Kekuda R, Pena CEA;
Zhong M, Gangolli EA, Taupier RJ;
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                                                                                                                                                                           Claim 1; Page 161; 266pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-FEB-2000; 2000EP-00301439,
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Best Local Similarity 77.8-
7; Conservative
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515 TRITKRGLE 523
                                                                  WPI; 2002-713508/77.
N-PSDB; ABS78750.
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RR 13-7UL-1999; 99US-0143542P

RR 15-7UL-1999; 99US-0144068P

RR 15-7UL-1999; 99US-0144068P

RR 19-7UL-1999; 99US-0144332P

RR 19-7UL-1999; 99US-0144332P

RR 20-7UL-1999; 99US-0144332P

RR 21-7UL-1999; 99US-0144332P

RR 21-7UL-1999; 99US-0144332P

RR 22-7UL-1999; 99US-014532P

RR 22-7UL-1999; 99US-014433P

RR 22-7UL-1999; 99US-014432P

RR 22-7UL-1999; 99US-014432P

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RR 22-7UL-1999; 99US-014932P

RR 22-7UL-1999; 99US-0151066P

RR 22-7UL-1999; 99US-0151069P

RR 22-7UL-1999; 99US-0151069P

RR 22-7UL-1999; 99US-015109P

RR 23-7UL-1999; 99US-015109P

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RR 24-7UL-1999; 99US-015109P

RR 24-7UL-1999; 99US-015109P

RR 24-7UL-1999; 99US-015109P

RR 24-7UL-1999
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gene disruption; gene targeting; marker gene; transformation; homologous recombination; hyperthermostable archaebacterium; KOD1; gene structure; gene function; enzyme activity; medicine; forensic science; food; drug inspection; molecular biology; immunology.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thermococcus kodakaraensis KOD1 protein sequence SeqID1384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADN47506 standard; protein; 238 AA.
99US-0157117P.
99US-015753P.
99US-0158029P.
99US-0158029P.
99US-0158232P.
99US-0159294P.
99US-0159294P.
99US-0159231P.
99US-0159331P.
99US-0159331P.
99US-0159331P.
99US-0159331P.
99US-0159634P.
99US-016091P.
99US-0160741P.
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99US - 0161359P.
99US - 0161359P.
99US - 0161361P.
99US - 0161920P.
99US - 0161992P.
99US - 0162142P.
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44 RFTKRGLK
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04-0CT-1999,
06-0CT-1999,
08-0CT-1999,
13-0CT-1999,
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12-0CT-1999,
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22-0CT-1999,
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22-0CT-1999,
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24-0CT-1999,
25-0CT-1999,
26-0CT-1999,
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ADN47506
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Claim 8; SEQ ID NO 6; 145pp; English.

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This invention relates to a novel method for targeting disruption of an arbitrary gene in a genome of an organism which comprises providing the whole sequential data of the genome of such organism, selecting at least a tabitrary region in the sequence, providing a vector that contains a remainder bemologous with the selected region and a marker gene, cransformation, and homologous recombination. The genome is preferably the genome of a hyperthermostable archaebacterium, particularly the genome of a penel in the genome of an organism, which is applicable in studying gene structure and functions as well as enzyme activities of encoded proteins and useful in medicine, forensic science, food or drug in spection, molecular biology and immunology. With this method, the disruption of a gene at an arbitrary position in a genome can be achieved efficiently and reliably. The present sequence is that of a protein concoded by the genome of Thermococcus kodakaraensis which was derived using the method of the invention. Note: The sequence data for this concoded format directly from MIPO at the sequence data for this format directly from WIPO at the invention.
                                                          Method for disrupting targeted gene in genome of organism particularly thermostable bacterium and with genome chips for analysis, applicable in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xanthomonas axonopodis pv citri plant pathology-related XAC3136 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 8; Length 238; Pred. No. 78; 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quaggio RB, Reinach FDC, F
ML, Setubal JC, Furlan LR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AMPA-) FUNDACAO AMPARO A PESQUISA DO ESTADO.
                                                                                                                                                                                              Claim 9; SEQ ID NO 1384; 598pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                studying gene structure and functions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADG30649 standard, protein, 335 AA.
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Oliveira JCF, De Laia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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WPI; 2004-257583/24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 238 AA;
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Ferro JA;

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                                     The invention relates to a novel isolated nucleic acid molecule from a Xanthomonas microorganism where the nucleic acid molecule is associated with pathogenicity caused by the Xanthomonas microorganism, or its variant, that causes reduced or enhanced pathogenicity. The nucleic acid of the invention may be useful in detecting the presence of Xanthomonas bacteria in a sample, as well as in plant pathology, for example, for caused by bacterial pests. The current sequence is that of the Xanthomonas axonopodis pv. citri (Xac) plant pathology-related XAC protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibite proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense encoding a city of a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gape
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Xu HH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 335;
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Forsyth RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein encoded by Prokaryotic essential gene #34307.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 7; I
Pred. No. 1.1e+02;
1; Mismatches 1;
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Yamamoto R,
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.38;
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Matches 7; Conservative
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294 TRLLERGLK 302
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Trawick JD,
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N-PSDB; ACA52650.
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 335 AA;
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proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for relular proliferation or the biological pathway is dentifying a gene required for calular proliferation or the biological dentifying a gene required for calular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent or to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids required for callular proliferation to isolate candidate molecules for rational card strains or screening for homologous mucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, CC and discovery programs, or for screening homologous mucleic acide by one of card discovery programs, or for screening the sequence is encoded by one of the traget prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained core the target prokaryotic segmented specification, but was obtained core the target proverse or the present directly from WIPO at the present directly from the present sequences.
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proliferation or the activity of a gene in an operon required for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.3%; Score 34; DB 6; Length 840; 87.5%; Pred. No. 2.9e+02; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR59926 standard; protein; 3079 AA.
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(first entry)
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Best Local Similarity 87.5
Matches 7; Conservative
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22-FEB-1995
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AAY30582-Y30700 represent apo-B100 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which modulate atheroseleroselerosis. The peptides are derived from amino acids 3358 to 3367 of apoB100. The method comprises detecting compounds which affect low density lipoprotein (LDL) binding with proteoglycan (PG). The method can be used for identifying compounds which disrupt LDL-FG binding without inhibiting LDL receptor binding. Such compounds can be used to reduce or prevent the formation of atherosclerotic lesions and prevent express human apo-B100 can be used as an in vivo model system for the study of atherosclerosis, and in vivo assay methods for identifying compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which modulate atherosclerosis and/or LDL-FG binding. They can also be used to identify compounds which result in an increase in atherosclerotic regions. Thus the assays may be used to determine whether a particular food or drug composition tends to stimulate or inhibit the committee of atherosclerotic regions. The polynucleotides can also be used in gene therapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                                                                                                                                                                                 ö
were located in one of the most conserved regions of GRD. These sites were compared with those of other GRD family proteins, yeast Ira2 (AAR59926) and Ira1 (AAR599313), human GAP (AAR5994) and Schizosaccharomyces pombe Gap1 (AAR59925). (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing
                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Apo-B100; proteoglycan receptor mutation; atherosclerosis; low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                                                                                                                                                                                 ö
                                                                                                                                                          Length 3079;
                                                                                                                                                                                               0; Indels
                                                                                                                                                        77.3%; Score 34; DB 2; Le
100.0%; Pred. No. 1.2e+03;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                      AAY30689 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 17; Page 57; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US004805.
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                                                                                                                                                                         Local Similarity 100.
Les 7; Conservative
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                                                                                                                                                                                                                                                                         3029 RLTKRGL 3035
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                                                                              correct PN field.)
                                                                                                                    Sequence 3079 AA;
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ID AAY3
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Sequence 10 AA;

Human neurofibromatosis type 1 (NP1)-GAP related domain (GRD) mutant clones NP201 (given in AAR59221) and NP204 (AAR59922) show strong suppression activity for RAGSVall9, and inhibit v-Ras-induced transformation in mammalian cells. The mutation sites of these proteins

Blocking Ras-induced effects on a cell - by introducing a GTPase activating protein to the cell, used esp. in treatment of cancers

Kaziro Y;

Nakafuku M,

WPI; 1994-249216/30.

Disclosure; Page 63-72; 87pp; English.

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us-09-823-418-14.rag

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Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                               AAW57205 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 12; Page 52; 73pp; English.
                                                                                                                                                  Apo B binding site peptide 2.
                                                                                                                                                                                                                                                                                                                                                                            (UYST ) UNIV STRATHCLYDE.
                                                                                                                                                                                                                                                                                                                                                                                                       Halbert GW, Owens MD,
1 TRLTEKRGLK 10
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                                                                                                                         03-AUG-1998
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                                                                                             AAW57205,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY30582-Y30700 represent apo-Bl00 derived peptides showing proteoglycan receptor mutations. They were created to identify compounds which computate atherosals. They were created to identify compounds which computate atherosals. The peptides are derived from amino acids 3388 to 3367 of apoBl00. The method comprises detecting compounds which affect can be used for identifying compounds which disrupt LDL-PG binding with proteoglycan (PG). The method compounds to the transgenic non-human animals and mammals which express human apo-Bl00 can be used an in vivo model system for the express human apo-Bl00 can be used as an in vivo model system for the express human apo-Bl00 can be used as an in vivo model system for the express human apo-Bl00 can be used and in vivo assay methods for identifying also be used to identify compounds which result in an increase in the about the assays may be used to determine whether can particular food or drug composition tends to stimulate or inhibit the formation of atherosclerotic lesions. The polynucleotides can also be used in gene thersapy for preventing or reducing the severity of atherosclerosis in an animal or mammal
                                    ı,
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying compounds which affect binding of low density lipoprotein with proteoglycan, used for, e.g. obtaining compounds for reducing atherosclerosis.
                                                                                                                                                                                                                                                                  Apo-B100; proteoglycan receptor mutation; atherosclerosis;
low density lipoprotein; proteoglycan; LDL; atherosclerotic lesion.
                                                                                                                                                                                                                                      Apo-B100 derived peptide showing a proteoglycan receptor mutation.
                                    1,
       DB 2; Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.1%; Score 33.5; DB 2; Length 10; 90.0%; Pred. No. 3.6; cive 0; Mismatches 0; Indels
                                 0; Indels
  Score 33.5; DB
Pred. No. 3.6;
0; Mismatches
                                                                                                                                                     AAY30688 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 17; Page 57; 70pp; English.
 76.1%;
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                                                                                                                                                                                                              (first entry)
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Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                  1 TRLTDKRGLK 10
                                                         1 TRLT-KRGLK
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                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                             17-NOV-1999
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                                                                                                                            RESULT 12
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Baillie

97WO-GB002610. 96GB-00020153

(first entry)

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The present sequence represents a specifically claimed Apo B binding site peptide which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (LDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 70% identity with sequences: KAEYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (1) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for call culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete apo B sequence, which is large and tends to aggregate, to provide binding caffinity to an apo B protein receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Сарв
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.1%; Score 33.5; DB 2; Length 11; 90.0%; Pred. No. 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 90.0
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axxxa
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Gaps

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1 TRLT-KRGLK 9

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prothrombinase complex.

Synthetic. Homo Bapiens. WO9743311-A1.

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The present sequence represents a specifically claimed Apo B 100 binding site peptide analogue which can be used as a component of a non-naturally occurring, receptor-competent low density lipoprotein (DDL) particle of the present invention. The LDL particle comprises at least 1 peptide component that has at least 1 binding site for an apo B protein receptor and at least 1 lipophilic substituent. Also described in the invention are peptides containing an apo B binding sequence with at least 10% identity with sequences: KARYKKNKHRH (1) or TTRLTRKRGLK (2), or their dimers. Non-naturally occurring, receptor-competent LDL particles are useful as: (i) drug-targeting vectors for delivering anticancer drugs to cancer cells that express an apo B protein receptor, and (ii) additives for cell culture media especially as growth supplements. Non-naturally occurring, receptor-competent LDL particles do not require the complete app B sequence, which is large and tends to aggregate, to provide binding
                                   Apo B; binding site; receptor; cancer; drug delivery; anticancer; growth supplement; non-natural lipid particle; low density lipoprotein; LDL; receptor component; apo B100 receptor site.
                                                                                                                                                                                                                                                                                                                                                                    Non-natural lipid particle comprising peptide binding to apo B protein receptor - useful as, e.g. vector for delivering drugs to cancer cells that express this receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anti-coagulant, apolipoprotein B-100, apoB-100; metastatic spread; thromboplastin-mediated process; cancer; inhibitor; blood coagulation; anglogenesis; cellular differentiation; apoptosis; KRAD-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.1%; Score 33.5; DB 2; Length 13; 90.0%; Pred. No. 4.7; ive 0; Mismatches 0; Indels
            Apo B 100 binding site peptide analogue peptide B.
                                                                                                                                                 /note= "attached to retinoic acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   affinity to an apo B protein receptor
                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  Baillie G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW41261 standard; peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 13; Fig 7; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apolipoprotein B-100 fragment.
                                                                                                                                                                                                                                                             96GB-00020153.
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                                                                                                                                                                                                                                                                                                                    Owens MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TRLTRKRGLK 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TRLT-KRGLK 9
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Best Local Similarity
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                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                             27-SEP-1996;
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                                                                                                                                                                            WO9813385-A2
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                                                                                                                                                                                                                                                                                                                  Halbert GW,
                                                                                            Synthetic.
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ID AAW4
XX AC AAW4
XX 19-h
XX XX BE Apol
XX Anti
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Peptide fragments of apo:lipo:protein B-100 with anticoagulant activity used for treating or preventing coagulation, inhibiting angiogenesis, cell differentiation and apoptosis.

Disclosure, Page 22, 60pp, English.

(UNLO) ROYAL FREE HOSPITAL SCHOOL MED.

Bruckdorfer KR, Ettelaie C;

WPI; 1998-008798/01.

97WO-GB001255 96GB-00009702

09-MAY-1997; 09-MAY-1996;

20-NOV-1997

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

December 29, 2004, 12:15:57; Search time 8.69118 Seconds (without alignments) 99.613 Million cell updates/sec Run on:

US-09-823-418-14 44 1 TRLTKRGLK 9 score:

Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		df			SUMMERLES	
Result		Query				
No.	Score	Match	Length	BB	qi	Description
-	36	81.8	427	7	A84155	hypothetical prote
7	35	79.5	631	7	T29926	hypothetical prote
3	34	77.3	66	7	A87912	u ı
4	34	77.3	248	~	877172	glucose dehydrogen
S	34	77.3	840	~	F82937	DNA topoisomerase
9	34	77.3	3079	-	RGBY12	probable GTPase-ac
7	33.5	76.1	296	N	S32802	apolipoprotein B -
89	۳.	76.1	4563	Н	LPHUB	apolipoprotein B-1
6		75.0		~	A11315	nucleoside diphosp
10	33	75.0	151	-	R3KW13	ribosomal protein
11		75.0		7	S39733	amino acid permeas
12	33	75.0		~	T05005	hypothetical prote
13	33	75.0		~	S51368	ribosomal protein
14	32	72.7		ч	ETHUL	lymphotactin precu
15	32	72.7	257	0	140170	hypothetical prote
16	32	72.7		~	G70179	쥖
17	32	72.7		~	S27422	peroxisomal assemb
18	32	72.7		N	A72253	c
19	32	72.7	306	~	T50120	hypothetical prote
20	32	72.7		Н	JH0185	
21	32	72.7		-	OXPGDA	D-amino-acid oxida
22	32	72.7	347	-1	S01340	D-amino-acid oxida
23	32	72.7	347	-	JX0132	D-amino-acid oxida
24	32	72.7	376	7	A98030	coproporphyrinogen
25	32	72.7	376	~	B95164	hypothetical prote
56	32	72.7	389	0	E96835	unknown protein F5
27	32	72.7	393	N	H75444	branched-chain ami
28	32	72.7	454	0	AG1977	hypothetical prote
53	32	72.7	625	N	B86875	metal transporting

poly Acet	hypothetical prote lymphotactin precu probable diphtheri	nypocnetical prote alanine racemase [hypothetical prote	ABC transporter pr dibydrolipoamide d	nypotnetical prote hypothetical prote Ras-binding protei	hypothetical prote probable sulfur me protein AC7.2 [imp
T07863 A59251	G81430 ETMSL C72769	T29841 C87455 AI2180	T17948 T44424	S18210 T25684 T42998	T30947 T38932 A88684
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330	ጋ ይ ይ ር ያ ር ት I	3 9 5 3 6 5	866	4 4 4 0 1 2	4 4 4 6 4 3

ALIGNMENTS

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RESULT 1
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hypotherical protein BH4041 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Bacillus halodurans
C;Species: Date: 00-lec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: A84155
R;Takani, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hir
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83550; MUID:20512582; PMID:11058132
A;Accession: A84155
A;Accession: A;Accession:

Gaps ö Length 427; 1; Indels Score 36; DB 2; Pred. No. 15; 1; Mismatches 81.8%; Query Match
Best Local Similarity 77.8
Matches 7; Conservative

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1 TRLTKRGLK 9 ઠે g

339 TRITKRGRK 347

hypothetical protein T03G11.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C; Accession: T29926
S; Gattung, S; Battung, S; Battung, November 1995
A; Description: The sequence of C. elegans cosmid T03G11.
A; Reference number: Z20709
A; Reference number: Z20709
A; Reference number: Z20709
A; Residues: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-631 < GEI>
A; Cross-references: UNIPROT: Q22126; EMBL: U41272; PIDN: AAA82452.1; CESP: T03G11.1

A;Gene: CESP:T03G11.1 A;Introns: 107/3; 214/3; 250/1; 306/2; 364/3; 405/2; 451/3; 522/1; 576/2

Query Match 79.5%; Score 35; DB 2; Length 631; Best Local Similarity 87.5%; Pred. No. 35; Matches 7; Conservative 1; Mismatches 0; Indels

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Gaps

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2 RLTKRGLK 9

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Richass, J.I.; Lefkowitz, B.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min A;Reference number: A82870
A;Accession: P82937
A;Status: preliminary
A;Molecule type: DNA
A;Residuse: 1-840 <cinA>
A;Residuse: 1-840 <cinA>
A;Coss-references: GB:AE002107; GB:AF222894; NID:g6899022; PIDN:AAF30487.1; GSPDB:GN0011
A;Experimental source: serovar 3; blovar 1
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A; Residues: 1-2423 <ZUNA
A; Residues: 1-2423 <ZUNA
A; Cross-references: UNIPROT: P19158; UNIPROT: O13592; EMBL: Z74823; GSPDB: GN00015; MIPS: YOL
A; Experimental source: strain S288C
R; Alexandraki, D.; Katsoulou, C.; Tzermia, M.
Bubmitted to the Protein Sequence Database, July 1996
A; Reference number: S66756
A; Accession: S66774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1983-3079 < ALE>
A; Residues: 1983-3079 < ALE>
A; Cross-references: EMBJ: 274823; GSPDB: GN00015; MIPS: YOL081w
A; Experimental source: strain $288C
A; Farnaka, K.; Nakafuku, M.; Tamanoi, F.; Kaziro, Y.; Matsumoto, K.; Toh-e, A.
Mol. Cell. Biol. 10, 4303-4313, 1990
A; Title: IRA2, a second gene of Saccharomyces cerevisiae that encodes a protein with a diagramment number: A35656; MUID: 90318397; PMID: 2164637
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A; Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>
A; Residues: 1-2308, 'V', 2310-2316, 'I', 2318-3079 <TAN>
A; Cross-references: EMBL.M33779; NID:g171761; PIDN:AAA34710.1; PID:g171762
B; Zumstein, E.; Griffin, H.; Schweizer, M.
Yeast 10, 1383-1387, 1994
A; Title: Sequence of a 10.27 kb segment on the left arm of chromosome XV from Saccharomy; A; Reference number: S48253; MUID:95208358; PMID:7900427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain A; phage T4 DNA topoisomerase
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A;Cross-references: EMBL:X75449; NID:g414079; PIDN:CAA53202.1; PID:g414081
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1993
R;Zumstein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
submitted to the EMBL Data Library, December 1994
A;Reference number: S50410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable GTPase-activating protein IRA2 - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Saccharomyces cerevisiae
C.Date: 30-Sep-1991 #sequence revision 16-Aug-1996 #text_change 09-Jul-2004
C.Paccession: S66775; S66774; A35856; S48284; S50426; S11190; S38505
R.Zumetein, E.; Pearson, B.M.; Kalogeropoulos, A.; Schweizer, M.
submitted to the Protein Sequence Database, July 1996
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, Status: nucleic acid sequence not shown; translation not shown
, Molecule type: DNA
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A;Genetic code: SGC3
C;Superfamily: DNA topoisomerase (ATP-hydrolyzing)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7
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Pred. No. 73;
0; Mismatches
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A,Status: nucleic acid sequence not shown
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Best Local Similarity 87.5
Matches 7; Conservative
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A, Molecule type: DNA
A, Residues: 1-2423 < ZU3>
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                                                                                                                                                                              Protein B0205.5 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L0.May-2010 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: A87912
R;anonymous, The C. elegans Sequencing Consortium.
C;Accession: A87912
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Nolecule type: DNA
A;Residues: 1-99 <STO>
A;Residues: 1-99 <STO>
A;Residues: 1-99 <STO>
A;Residues: 1-99 <STO>
A;Consorreferences: UNIPROT:O61740; GB:chr_I; PIDN:AAC16987.1; PID:g3150469; GSPDB:GNOOG
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A.Reference number: S77172
A.Status: nucleic acid sequence not shown, translation not shown
A.Molecule type: DNA
A.Residuss: 1-248 <KAN>
A.Residuss: 1-248 <KAN>
A.Cross-references: UNIPROT:P73684; EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA1773
A.Cross-references: Uniprocence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rikaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA topoisomerase chain A, DNA gyrase A subunit UU082 [imported] - Ureaplasma urealyticu
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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A;Gene: gdh
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;6-186/Domain: short-chain alcohol dehydrogenase homology <SADH>
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N/Alternate names: protein sll1709
C/Species: Synechocystis sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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Pred. No. 9.8;
3; Mismatches
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Best Local Similarity 66.7
Matches 6; Conservative
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Matches 7; Conservative
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539 RLTKQGLK 546
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C/Genetics:
A/Gene: B0205.5
A/Map position: 1
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A; Molecule type: mRNA
A; Residues: 1-291 < PRO>
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R;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchid B;Pape, M.E.; Castle, C.K.; Murray, R.W.; Funk, G.M.; Hunt, C.E.; Marotti, K.R.; Melchid Biochim. Biophys. Acta 1086, 328-334, 1991
A;Title: Apo B metabolism in the cynomolgus monkey: evidence for post-transcriptional refarence number: S32802; MuID:92075708; PMID:1742325
A;Accession: S32802
A;Coss-references: UNIPROT:028473; EMBL:X15737; NID:g38047; PIDN:CAA33755.1; PID:g93012
C;Superfamily: apolipoprotein B
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C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text change 09-Jul-2004
C;Accession: A27850; A25679; A25263; A25265; A24320; A24684; A23817; A26452; I61909; I59510; I39474; I33469; I84644; I37179; PS0058
R;Ludwig, E.H.; Blackhart, B.D.; Pierotti, V.R.; Caiati, L.; Fortier, C.; Knott, T.; Sco
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A, Molecule type: DNA
A, Molecule type: DNA
A, Rolecule type: DNA
A, Rolecule type: DNA
A, Crosd-references: UNIPROT: P04114; UNIPROT: P78482; UNIPROT: P78479; UNIPROT: O9UMNO; UNIF
R, Cladaras, C.; Hadzopoulou-Cladaras, M.; Nolte, R.T.; Atkinson, D.; Zannis, V.I.
EMBO J. 5, 3495-3507, 1986
A, Title: The complete sequence and structural analysis of human apolipoprotein B-100: re
A, Reference number: A91058; MUID: 87161758; PMID: 3030729
                                                                                                                                                                     Superfamily: regulatory protein IRA2; ras-specific GAP catalytic domain homology Keywords: transmembrane protein ;693-709/Domain: transmembrane #status predicted <TM1>
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C'Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
A; Cross-references: EMBL: X83121; NID: 9600461; PIDN: CAA58201.1; PID: 9600480
                                                                                                                                                                                                                                                                            Fill35-1151/Domain: transmembrane #status predicted <TM2>
Fil701-1910/Domain: ras-specific GAP catalytic domain homology <GAP>
Fil842-1858/Domain: transmembrane #status predicted <TM3>
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A;Residues: 1-11,15-2539,'S',2541-3823,'R',3825-4563 <CLA>
A;Note: 1109-Asp was also found
                                                                                                                                                                                                                                                                                                                                                  F;1842-1858/Domain: transmembrane #status predicted <TM3>F;2318-2334/Domain: transmembrane #status predicted <TM4>F;2562-2578/Domain: transmembrane #status predicted <TM5>
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A;Reference number: A27850; MUID:88003974; PMID:3652907
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Pred. No. 67;
0; Mismatches
                                            A;Gene: SGD:IRA2; MIPS:YOL081w
A;Cross-references: SGD:SO005441; MIPS:YOL081w
A;Map position: 15L
C;Superfamily: regulatory protein IRA2: ras-en
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Best Local Similarity 90.0
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Matches 7; Conserv
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A;Residues: 28-41;76-97,′I′,99-100;175-193;206-215;239-249;259-266;357-399;455-490;512-5
                                                                                                                                 A;Note: cysteines at positions 1112, 1422, 1505, 1662, 3761, 3917, and 4217 have free su FreeGouf, R.C.; Miller, C.; Shively, J.E.; Schumaker, V.N.; Balla, M.A.; Lusis, A.J. PEBS Lett. 170, 105-108, 1984 4.3 A.J. A;Title: Human apolipoprotein B: partial amino acid sequence.
A;Reference number: A22006; MUID:84208786; PMID:6373369
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B;Molecule type: protein
B;Molecule type: protein
A;Molecule type: protein
B;Molecule type: protein
B;Molecule type: protein
A;Molecule type: protein
B;Molecule type: prot
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C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C;Accession: Al1315
S;Accession: Al1315
S;Accession: D: Duchaud, E.; Duchaud, A.; Baquero, F.; Berche, P.; Bloecker.
D: Jones, L.M.; Karst, U.
D: Jones, L.M.; Karst, U.
D: Jones, L.M.; Karst, U.
A;Authors: Kreft, J.; Kuhn, M.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mayathors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-147 <GLA>
A;Cross-references: UNIPROT:Q8Y5X4; GB:NC_003210; PIDN:CAD00007.1; PID:g16411382; GSPDB
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C, Genetics:
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Best Local Similarity
Matches 9; Conserv
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                                           A;Cross-references: Gi:Mi73-7: NID:g178731; PIDN:AAA51741.1; PID:g178732
R;Shoulders, C.C.; Myant, N.B.; Sidoli, A.; Rodriguez, J.C.; Cortese, C.; Baralle, F.E.; Ahrerosclerosis 58, 277-289, 1985
A;Title: Molecular cloning of human LDL apolipoprotein B cDNA. Evidence for more than on A;Reference number: A90084; MUID:86130855; PMID:3841481
                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 3846-4298 CSHO>
R; Pfitzner, R; Wagener, R.; Stoffel, W.
Biol. Chem. Hoppe-Seylar 367, 1077-1083, 1986
A; Title: Isolation, expression and characterization of a human apolipoprotein B 100-spec
A; Reference number: A25572; MUID:87076044; PMID:3024665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Molecule type: mRNA
A.Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
A.Residues: 'N',3729-3731,'I',3733-3875,'A',3877-3948,'F',3950-3963,'Y',3965-3982,'S',39
A.Crose-references: GB.M12413; NID:9778735; PIDN:AAA51742,1; PID:9178736
B.Crose S.H.; Habib, G.; Yang, C.Y.; Gu, Z.W.; Lee, B.R.; Weng, S.; Silberman, S.R.; Cai
A.Title: Apolipoprotein B-48 is the product of a messenger RNA with an organ-specific in
A.Reference number: A40133; MUID:88018019; PMID:3659919
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A/Molecule type: protein

36,1486-1498,1537-1556,101-110,129-139,158-174,197-207;276-287;298-304;306-314;526-532;538-55

36,1486-1498;1537-1556,1563-1572,1601-1610,1647-1661,1697-1724;1770-1781;1859-1897;1968-

A/Note: these fragments were derived from 50.00 J.W.; Kane, J.P.

Biochem Blophys Res. Commun. 149, 1214-1219, 1987

A/Title: Carboxyl terminal analysis of human B-48 protein confirms the novel mechanism p

A/Reference number: A28002; MUID:88106542; PMID:3426612
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A, Residues: 2169-2179 <HOS>
A, Residues: 2169-2179 <HOS>
A, Residues: 2169-2179 <HOS>
A, Note: the sequence shown represents the carboxyl end of apolipoprotein B-48
A, Note: two RNA species, 14.1kb and 7.5kb in length, were isolated from the human intest chencodes the 250k apoB-48, CAA encoding 2180-din is substituted by the stop codon TAA, Proc. Natl. Acad. Sci. US.A. 87, 5523-5527, 1990
A, Title: Isolation and characterization of sulfhydryl and disulfide peptides of human ap A, Reference number: A35783; MUD: 90319144; PMID:2115173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Readdues: 4219-4317, S;,4339-4563 <PFI>
A;Cross-references: GB:MA6676
R;Wei, C.F.; Chen, S.H.; Yang, C.Y.; Marcel, Y.L.; Milne, R.W.; Li, W.H.; Sparrow, J.T.
Proc. Natl. Acad. Sci. U.S.A. 82, 7265-7269, 1985
A;Reference number: A24738; MUID:86042646; PMID:2932736
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| Residues: 1219-1219, 1281-2235 < HA2>
| Residues: 1219-1219, 1281-2235 < HA2>
| Residues: 1219-1219, 1281-2235 < HA2>
| Experimental source: Intestine
| RNA from intestine includes a stop codon created by RNA editing in place
| Note: this mRNA from intestine includes a stop codon created by RNA editing in place
| Note | Robinson, M.; Schumaker, V.N.; Fareed, G.C.; West, R.; Johnson, D.F.; Kirchgessner, and leit Acids Res. 13, 6937-6953, 1985
| Fatter | Robinsoprotein B: identification of cDNA clones and characterization of Reference number: A24269; MUID:86041888; PMID:3903660
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A,Residues: 2165-2179 <CH1>
A,Residues: 2165-2179 <CH1>
A,Cross-references: GB:M18036; NID:g178799; PIDN:AAA51754.1; PID:g178800
A,Note: this mRNA includes the stop codon of the organ-specific mRNA for apo48
A,Accession: A40133
A,Residues: 1671-2323,'PYW',2327-2352,'H'
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A;Molecule type: protein
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i,

75.0%; Score 33; DB 2; Length 147;

Query Match

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y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetell Rieger. M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon A, Authors. Schleich, G.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Tangkra, P.; Tognoni, A.; Tosato, V.; Uchiyama A, Authors. P.; Winters, P.; Wipat, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Voshida, A, Althors. Voshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A. A, Accession. G69693
A, Reference number: A69580; MUID:98044033; PMID:9384377
A, Residues: Dreliminary; nucleic acid sequence not shown; translation not shown A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-470 cKUN>
A, Residues: 1-470 cKUN>
A, Resperances: GB:Z99123; GB:AL009126; NID:g2636240; PIDN:CABIS803.1; PID:g26363312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T19P19.70 - Arabidopsis thaliana (Species Arabidopsis thaliana (mouse-ear cress) (Species Arabidopsis thaliana (mouse-ear cress) (S. Species 13-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 (S. Accession: T0S005 (Mouse) (M
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Cutr. Genet. 27, 54-61, 1994
A.Title: The chloroplast gene cluster containing pabF, pabL, petG and rps3 is conserved A.F.Reference number: 851365; MUID:95269309; PMID:7750147
A.A.Cocsesion: 851368
A.Molecule type: DNA
A.Residues: 1-800 <TUR>
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C;Species: chloroplast Chlamydomonas eugametos
C;Date: 01-Aug-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S51368
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C;Keywords: amino acid transport; glycoprotein; transmembrane protein
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Pred. No. 68;
2; Mismatches
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0; Mismatches
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Pred. No. 9
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87.5%;
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A;Introns: 385/1; 448/1; 498/3
A;Note: T19P19.70
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity 87.5
Matches 7; Conservative
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A,Gene: rps3
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Cispeciae: Bacillus subtilis
NiAlternate names: protein ipa-77d
Cispeciae: Bacillus subtilis
Cipate: 07-Oct-1994 #Bequence_revision 26-May-1995 #text_change 09-Jul-2004
Cispeciae: Bacillus subtilis
Cipate: 07-Oct-1994 #Bequence_revision 26-May-1995 #text_change 09-Jul-2004
Cispeciae: Bacillus subtilis
Riglacer, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A;Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr A;Reference number: 839655; MUID:95020537; PMID:7934828
A;Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region fr A;Reference number: 839655; MUID:95020537; PMID:7934828
A;Reference number: 839655; MUID:95020537; PMID:7934828
A;Reference number: Signature or degenence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-470 cGLA
A;Residues:
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A,Mocession: 332687
A,Mocession: 332687
A,Rocession: 332687
A,Mocession: Size By A,Residues: 1.151 CELL>
A,Cross-references: UNIPROT:017274; EMBL:X63714; NID:g297070; PIDN:CAA45247.1; PID:g2970
R,Ellenberger, D.L.; Pieniazek, N.J.; Lammie, P.J.
Nucleic Acids Res. 17, 10121, 1989
A,Title: Nucleotide sequence of Brugia pahangi 17.4 kD protein.
A,Reference number: S14440; MUD:90098795; PMID:2602125
A,Residues: 12440
A,Mocession: S14440; MUD:90098795; PMID:2602125
A,Residues: 1-26, KK',28-36, VV,38-106, 'Q',108-118, 'Q',120-123,'R',125-151 <EL2>
A,Genetics:
A,Introns: 43/3; 78/3; 107/3
C,Superfamily: rat ribosomal protein S13; eubacterial ribosomal protein S15 homology
C,Superfamily: rat ribosomal protein S13: #status predicted <MAT>
F,82-148/Domain: eubacterial ribosomal protein S15 homology <ES15>
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ribosomal protein S13.e, cytosolic - nematode (Brugia pahangi)
NyAlternate names: 17.4K protein
C;Species: Brugia pahangi
C;Species: Brugia pahangi
C;Date: 30.58p-1991 #sequence revision 19.Apr-1996 #text_change 09.Jul-2004
C;Accession: S32687; S1440; S06771
K;Ellenberger, D.L.; Pleniazek, N.J.; Lammie, P.J.
Submitted to the EMBL Data Library, January 1992
A;Description: Developmental modulation of relative gene numbers in a parasitic nematode
A;Reference number: S32687
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Pred. No. 23;
2; Mismatches
             d. No. 23;
Mismatches
                  Pred. No.
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         66.7%;
                                                       6; Conservative
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Matches 6; Conservative
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TRIEKKGLK 31
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TRLAKKGLR 46
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129 QLTKRGVK 136
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61 ITKRGLK 67
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NiAlternate names: activation-induced chemokine-related protein (ATAC); single cysteine
NiAlternate names: activation-induced chemokine-related protein (ATAC); single cysteine
C;Sociations: eosinophilotactic peptide
C;Sociations (man)
C;Date: 23-Oct-1981 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
C;Accession: 860650; 189978; A03190; 153506
R;Muchler, S; Dorner, B; Korthaeuer, U; Mages, H.W.; D'Apuzzo, M.; Senger, G.; Krocze
Eur. J. Immunol. 25, 1744-1748, 1995
A;Fitle: Cloning of ATAC, an activation-induced, chemokine-related molecule exclusively
A;Fitle: Cloning of ATAC, an activation-induced, chemokine-related molecule exclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Molecule type: mRNA
A;Residues: 1-114 <MUE>
B;Cross-references: UNIROT: P47992; EMBL:X86474; NID:g895846; FIDN:CAA60198.1; PID:g8958
B;Kennedy, J; Kelner, G.S.; Kleyensteuber, S.; Schall, T.J.; Weiss, M.C.; Yssel, H.; Sc J. Immunol. 155, 203-209, 1995
A;Title: Molecular cloning and functional characterization of human lymphotactin.
A;Reference number: 138978; MUID:95325590; PMID:7602097
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A; Attacus: translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-114 «KEN»
A; Cross-references: EMBL: U23772; NID: 9902001; PIDN: AAC50164.1; PID: 9902002
B; Goetzl, E.G.; Austen, K.F.
Proc. Natl. Acad. Sci. U.S.A. 72, 4123-4127, 1975
A; Title: Purification and synthesis of eosinophilotactic tetrapeptides of human lung tis
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C;Comment: Lymphotactin is produced by activated T-cells and is chemotactic for some lym C;Comment: Eosinophilotactic peptide is released from mast cells in lung and other tissu ially affecting eosinophils, include chemotaxis, chemotactic deactivation, release of en C;Comment: It has not yet been shown that the previously detected eosinophilotactic peptide.
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A/Residues: 22-25 <GOS>
A/Residues: 22-25 <GOS>
A/Residues: 22-25 <GOS>
A/Residues: 22-25 <GOS>
A/Rote: 22-Also seen
R/Yoshida, T.; Imal, T.; Kakizaki, M.; Nishimura, M.; Yoshie, O.
R/Yoshida, T.; Imal, T.; Kakizaki, M.; Nishimura, M.; Yoshie, O.
A/Rile: Molecular cloning of a novel C or gamma type chemokine, SCM-1.
A/Reference number: 153506, MUID:95180438; PMID:7875320
A/Reference number: 153506

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                                                                                                   75.0%; Score 33; DB 2; Length 800; 77.8%; Pred. No. 1.1e+02; Conservative 1; Mismatches 1; Indels
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Pred. No. 29;
1; Mismatches 0; Indels
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C, Keywords: chloroplast; protein biosynthesis; ribosome
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A;Map position: 1q23-1q25
C;Superfamily: lymphotactin
C;Keywords: chemotaxis; cytokine; I:P:1-15/Domain: signal sequence Hera
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266 TKLTKRQLK 274
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                                                                                         Query Match
Best Local Similarity
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Rightm, S.Y.; Neubard, J.

J. Bacteriol. 176, 3698-3707, 1994

A. Accession: 140170

A. Accession: 140170

A. Accession: 140170

A. Fatatus: preliminary; translated from GB/EMBL/DDBJ

A. Residues: 1-257 crss

A. Residues: 1-257 crss

A. Cross-references: UNIPROT: P46536; EMBL: X73308; NID: 9312439; PIDN: CAA51740.1; PID: 93124|
C. Superfamily: cytochrome-c3 hydrogenase gamma chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
hypothetical protein 2 - Bacillus caldolyticus
C;Species Bacillus caldolyticus
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Jul-2004
C;Accession: I40170; S34322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 257;
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Pred. No. 62;
2; Mismatches
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Best Local Similarity 75.0%;
Matches 6; Conservative
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Bad18271 bacillus

Qécide kluyveromyc Qeghis brachydanio Qeghis brachydanio Qetys5 brachydanio Qetys7814 brachydan Qefy184 wolbachia p Aasta361 wolbachia p Aasta361 wolbachia p P73684 gynechocyst Qeme72 parachlamyd Caf53127 parachlamyd Caf53127 parachlamyd Caf53127 parachlamyd Qephw2 xanthomonas Qephw2 ureaplasma

Scoring table:

Searched:

Database

Perfect score: Sequence:

Title:

Run on:

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FIRAINEQUEGIA;

MEDLINE=22753791; PubMed=12730200;

MEDLINE=22753791; PubMed=12730200;

Parschat K., Hauer B., Kappl R., Kraft R., Huettermann J., Fetzner S.;

The construction of the Arthrobacter ilicis R. 61a Involved in the Degradation of Quinaldine to Arthrobacter ilicis R. 61a Involved in the Degradation of Quinaldine to Arthranilate. Characterization and Functional Expression of the Quinaldine 4-oxidase qoxLMS Genes.";

J. Biol. Chem. 278:27483-27494 (2003).

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:0006810; P:transport; IEA.

InterPro; IPR00714; MFS.

PROSITE; PSS0850; MFS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves; Neognathae, Galliformes; Phasianidae, Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arthrobacter ilicis. Bacteridae, Actinomycetales, Bacteria, Actinobacteria, Antinobacteria, Micrococcineae, Micrococcineae, Micrococcineae, Micrococcineae, Micrococcineae, Arthrobacter.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
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Pred. No. 8.3;
1; Mismatches
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GYRA_UREPA
                Q6CLD8
Q8QH18
Q8QH17
Q6TGXS
AAQ97814
O61740
Q73HA4
AAS14361
P73684
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88.9%;
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 86.2...
Best Local Similarity
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207 TRLTKOGLK 215
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01-OCT-2003 (
01-OCT-2003 (
   Name=PPA
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Q8QH16,
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Q8bid8 mus musculu
Q8nle6 homo sapien
Q75tw9 bacillus ha
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                                                                                                                   December 29, 2004, 12:13:11 ; Search time 52.5682 Seconds (without alignments) 98.508 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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FXLE_MOUSE
FXLE_HUMAN
Q75TW9
BAD18188
Q75TN6
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Maximum Match 100%
Listing first 45 summaries
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Q75TX7
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

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Balake J.A., Bradt D., Brusic V., Chothia C., Corbani D.E., Cousins S.,

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RA Gassterland T., Gartboldd M., Gissel C., Godzik A., Frazer K.S.,

RA Gasterland T., Rawasawa Y., Kedzierski R.M., King B.L.,

Konagaya A., Kurochkin I.V., Lee Y., Lehmard B., Lyons P.A.,

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Magashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

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Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,

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Sultana R., Wanner L., Wahlestedt C., Wang Y., Watnaba K.,

Numa Z., Zavolan M., Zhu Y., Zimmer A., Secou M., Shimada K.,

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Miyazaki A., Sakai K., Sasaki D., Sahbata R., Shibata K., Shinagawa I.,

Miyazaki A., Sakai K., Sasaki D., Shibata K., Shibata K., Shipata K., 
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QBBIDB; QBR5H7; QBVDT7; Q922NS;
QBSIDB; QGR6H. 44, Created)
05-JUL-2004 (Rel. 44, Last auroration update)
05-JUL-2004 (Rel. 44, Last annotation update)
F-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
MEDLINE=21972450; PubMed=11976951;
Das T., Purkayastha-Mukherjee C., D'Angelo J., Weir M.;
"A conserved F-box gene with unusual transcript localization.";
Dev. Genes Evol. 212:134-140(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                          86.4%; Score 38; DB 2; Length 188; 77.8%; Pred. No. 9.6; tive 2; Mismatches 0; Indels
                                                                                                                      Das T.K., Purkayastha-Mukherjee C., D'Angelo J., Weir M.; Das T.K., Purkayastha-Mukherjee C., D'Angelo J., Weir M.; Submitted (DEC-2001) to the EMBL, GenBank/DDBJ databases. EMBL, AF67646; AAL75968.1; -InterPro; IPR001611; LRR. InterPro; IPR001611; LRR. InterPro; IPR007089; LRR. Cys.
                                                                                                                                                                                                                                                                                                                                                188 189 20629 MW; 21702832DA5CE865 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 77.8 tes 7; Conservative
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
A Tausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
A Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonsloom R.D., Mullahy S.J.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
A Nodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Schalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
A Scherzation and initial analysis of more than 15,000 full-length human
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43864 MW; E0B297E4B4F83C22 CRC64;
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--- SIMILARITY: Contains 1 F-box domain.
--- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
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Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches
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LRR 2.
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PROSITE; PS50181; FBOX; FALSE_NEG.
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InterPro; IPR001810; F-box.
InterPro; IPR001611; IRR.
InterPro; IPR008995; Skpl_Skp2.
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SEQUENCE OF 207-390 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and mouse cDNA sequences."
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Pfam; PF00560; LRR; 6.
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400 AA;
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418 AA; 45886 MW; 5779961C8177779F CRC64;

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MEDLINE=223825; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Heish F.,
A Diatchenko L., Judin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Misceley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-- FUNCTION: Probably recognizes and binds to some phosphorylated
proteins and promotes their ubiquitination and degradation.

-- SUBUNIT: Part of a SCF (SKP1-cullin-F-box) protein ligase complex
                                                                                                                                                                              05-JUL-2004 (Rel. 44, Created)
05-JUL-2004 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
P-box/LRR-repeat protein 14 (F-box and leucine-rich repeat protein
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (By similarity).
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
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REPEAT 20 110 LRR 1.

REPEAT 203 231 LRR 2.

REPEAT 204 LRR 3.

REPEAT 254 280 LRR 4.

REPEAT 331 356 LRR 6.
                                                                                                                                 418 AA.
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InterPro; IPR01810; F-box.
InterPro; IPR001611; I.RR.
InterPro; IPR007089; I.RR.
Pfam; PP00646; F-box; 1.
Pfam; PP00560; I.RR.
SMART; SM00256; FBOX; 1.
PROSITE; PS50181; FBOX; FALSE_NEG.
                                                                                                                               PRT;
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                                                                                                                               STANDARD;
367 TRITKRGLE 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                               Name=FBXL14;
                                                                                                                         FXLE HUMAN QBN1\overline{E}6;
                                                                                                      FXLE HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AH-101;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Magui Takami H., Nakasone K., Takaki Y., Ogasawara N., Kuhara S., Horikoshi K.;
              Score 38; DB 1; Length 418;
Pred. No. 22;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.8%; Score 36; DB 2; Length 423; 77.8%; Pred. No. 60;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126496; BAD1818981; -.
InterPro; IPR00346; Transposase 20.
InterPro; IPR002525; Transposase 20.
Ffam; PF0271; Transposase 20.
Pfam; PF0281; Transposase 20.
Pfam; PF01848; Transposase 9; 1.
SEQUENCE 423 AA; 48264 WW; 72B7EDDE480E9BAO CRC64;
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Last annotation update)
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                     86.4%;
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Query Match
Best Local Similarity 77.5-
7, Conservative
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05-JUL-2004 (TrEMBLrel.
05-JUL-2004 (TrEMBLrel.
                                                                                                                                         367 TRITKRGLE 375
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                                                                                                   1 TRLTKRGLK 9
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Transposase of IS653
                                                                                                                                                                                                                                                                                                                                                                 ORFNames=BH9065301;
Bacillus halodurans
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PubMed=11418576;
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01-JUN-2004
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BAD18188;
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BAD18188
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(NOV-2003) to the EMBL/GenBank/DDBJ databases
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Matches 7; Conservative
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SEQUENCE FROM N.A.
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Q75TQ1,
05-JUL-2004 (
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                                                                                                                                                           Takami H., Han C., Takaki Y., Ohtsubo E., Indentification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                             STRAIN-AH-101,
BEDLINE-26512582; PubWed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasswara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM12;
Pubmed-11418576;
Takami H., Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=AH-101;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Wide-range distribution of insertion sequences identified in B. halodurans among bacilli and a new transposeon disseminated in alkaliphilic and thermophilic bacilli.";
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126496; BAD18188.1;
SEQUENCE 423 AA; 48264 MW; 72B7EDDE480E9BAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-DSM12;
MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Fakami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Takami H., MatBuki A., Takaki Y.;
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ORFNames=BF1065301;
Bacillus firmus.
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                                                                  SEQUENCE FROM N.A.
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         NCBI_TaxID=86665;
                                                                                               STRAIN=AH-101;
PubMed=11418576;
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Takani H., Han C., Takaki Y., Ohtsubo E.;
Tidentification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
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MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transposase of IS650 (Transposase of IS653).
0RFNames=BAL065001, BAL065301;
Bacillus alcalophilus.
Bacillus pirmicutes; Bacillales; Bacillaceae; Bacillus.
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Takani H., Matsuki A., Takaki Y.;

Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AB126557; BAD18256.1; -.

InterPro; IPR003346; Transposase_20.

InterPro; IPR003255; Transposase_20.

Fam: PF02371; Transposase_20.

Pfam: PF02371; Transposase_20; 1.

Pfam: PF02371; Transposase_20; 1.

SEQUENCE 427 AA; 48754 MW; B3B77D309F000033 CRC64;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases EMBL; AB126567; BAD18271.1; -.
InterPro: IPR003346; Transposase 20.
InterPro: IPR002525; Transposase 20.
Pfam; PR02371; Transposase 20; 1.
Pfam; PF01548; Transposase 20; 1.
SEQUENCE 427 AA; 48654 MW; B812714B694F3C88 CRC64;
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77.8%; Pred. No. 60;
iive 1; Mismatches 1
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Takami H., Han C., Takaki Y., Ohtsubo E.; "Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125."; J. Bacteriol. 183:4345-4356(2001).
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"Identification and distribution of new insertion sequences in the
genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
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Makani H., Nakagone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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NCBI_TaxID=86665;
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AB126489; BAD181181.1;
InterPro; IPR003346; Transposase 20.
InterPro; IPR003546; Transposase 20.
Ffam; PF02371; Transposase 20.
Ffam; PF02371; Transposase 20.
Ffam; PF01548; Transposase 20.
EMBL, ABP01541; Transposase 20.
EMBL, ABP01548; Transposase 20.
EMBL, ABP01548; Transposase 20.
EMBL, ABP01548; Transposase 30.1.
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Takaml H., Matsuki A., Takaki Y.;
Submitted (NOV-2013) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126492; BAD16184.1; -.
InterPro; IPR003346; Transposase_20.
InterPro; IPR00325; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
SEQUENCE 427 AA; 48726 WW; ED574C892EC CRC64;
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Best Local Similarity 77.8%; Pred. No. 60;
Matches 7; Conservative 1; Mismatches
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Best Local Similarity
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Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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MEDLINE-20512582; PubMed=11058132;
MEDLINE-20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
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Takami H., Mateuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126494; BAD18186.1; -.
                                                                                                                                                                                     Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=86665;
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InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
Pfam; PF01548; Transposase_9; 1.
SEQUENCE 427 AA; 48724 WW; 332EAB0F1B1815A0 CRC64;
      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transposase of IS653.
ORFNames=BH7065301;
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Matches 7; Conservative
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ORFNames=BH5065301;
Bacillus halodurans.
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PubMed=11418576;
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PubMed=11418576;
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PubMed=11418576;
Takami H., Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Takami H., NakaBone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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Pred. No. 60;
1; Mismatches 1; Indels
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STRAIN=DSW497;
Takami, H., Matsuki, A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB126468; BAD18180.1; -.
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NCBI _TaxID=86665,
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NCBI_TaxID=86665;
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                                                                      05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Transposase of IS653 (Transposase of IS650)
ORFNames=BH1065001, BH1065301;
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                                                         427 AA
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InterPro; IPR003525; Transposase 9.
Pfam; PF02371; Transposase 20; 1.
SEQUENCE 427 AA; 48754 WW; B3B77
                                                        PRT;
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05-JUL-2004 (TrEMBLrel. 27, Le
05-JUL-2004 (TrEMBLrel. 27, Le
Transposase of ISS50.
ORFNames=BH806501;
Bacillus halodurans.
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Local Similarity 77.8%;
les 7; Conservative 1
                                                      PRELIMINARY;
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339 TRITKRGRK 347
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                                                                                                                                Bacillus halodurans.
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Horikoshi K.;
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SEQUENCE
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Q75TZ5,
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"Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                              PubMed=11418576;
PubMed=11418576;
Takami H., Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
J. Bacteriol. 183:4345-4356(2001).
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STRAIN=DSM8718, DSM9774, and DSM6939;
STRAIN=DSM87185,
Tabmed=11, Han C., Takaki Y., Ohtsubo E.;
"Identification and distribution of new insertion sequences in the genome of alkaliphilic Bacillus halodurans C-125.";
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STRAIN=DSM8718, DSM9774, and DSM6939;
STRAIN=DSM8718, DSM9774, and DSM6939;
MEDLINES-20512582; PubMed=11058132;
MEDLINES-20512582; PubMed=11058132;
Makasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
1Tanspoase of IS650 (Transposse of IS653).
0RFNames=BH4065001, BH4065301, BH6065301, BH6065301,
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Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

BMBL, AB126470; BMD18162-1;

InterPro; IPR003346; Transposase 20.

Pfam; PF02371; Transposase-20.

Pfam; PF02371; Transposase-3.

Pfam; PF02371; Transposase-9.

Pfam; PF0248; Transposase-8.

SEQUENCE 427 AA; 48726 MW; 14692A5DC572A2B8 CRC64;
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Takami H., Matsuki A., Takaki Y.;
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 60;
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EMBL, AB126469, BAD1816011;
EMBL, AB126491, BAD1818311;
EMBL, AB126493, BAD1818311;
EMBL, AB126466, BAD1815811;
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Tabami H., Han C., Takaki Y., Ohtsubo E.;
Tabami H., Han C., Takaki Y.;
Takami H., Matsuki A., Takaki Y.;
Takami H., Matsuki Transposase 20.
Takami PF02371; T
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STRAIN=DSM6940;
MBDLINE=20512582; PubMed=11058132;
MBDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317-4331(2000).
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81.8%; Score 36; DB 2; Length 427;
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Matches 7; Conservative 1; Mismatches 1; Indels
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ORFNames=BH5065001;
Bacillus halodurans
Bacteria; Firmicutes; Bacillales; Bacillus
InterPro; IPR003346; Transposase_20.
InterPro; IPR002525; Transposase_9.
Pfam; PF02371; Transposase_20; 1.
Pfam; PF01548; Transposase_9; 1.
SEQUENCE 427 AA; 48696 WW; F14A&D5B2B009CB8 CRC64;
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